

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: October 7, 2003, 07:12:03 ; Search time 1 Seconds
(without alignments)
1.939 Million cell updates/sec

Title: us-10-053-510-8
Sequence: 2977
1 MPSTDLMKAFEPYELILE.....LYSTDVTGSGQNGSPKPH 568

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1 segs, 1707 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1 summaries

Command line parameters:
-MODEL-frame+ p2n.model -DEV-soft -O-us-10-053-510-8 -DB-us-10-053-510-7
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-START=1 -END=1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST=1 -DOCALIGN=200
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-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : us-10-053-510-7:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length DB	ID	Description
1	2977	100.0	1707	1 us-10-053-510-7

ALIGNMENTS

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us-10-053-510-7
Alignment Scores:
Pred. No.: 0
Score: 2977.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 100.00%
DB: 1
Length: 1707
Matches: 568
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

us-10-053-510-8 (1-568) x us-10-053-510-7 (1-1707)

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Qy 41 GlnLeuIleAlaTrpSerValValTrpThrLeuLeuIleValTrpGlyTyrGluPheVal 60
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Qy 101 LysAsnMetSerPheLeuLysValAspLysGluTyrValLysAlaLeuProSerGlnGly 120
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Qy 121 LeuSerSerSerAlaValLeuGluLysLeuLysGluTyrTrpSerSerMetAspAlaPheThr 140
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Qy 141 GlnGluGlyArgAlaSerGlyThrValTrpSerGlyGluGluLysLeuThrGluLeuLeu 160
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Db      1681 ATGAATGGTTCTCCAAAMCCCCAC 1704
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Search completed: October 7, 2003, 07:12:07
Job time : 4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using SW model

Run on: October 6, 2003, 12:29:09 ; Search time 109 Seconds
(without alignments)
6912.303 Million cell updates/sec

Title: US-10-053-510-7
Perfect score: 1707
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_MA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1707	100.0	1707	US-09-849-180-3	Sequence 3, Appl
3	1707	100.0	1707	US-09-356-643B-7	Sequence 7, Appl
4	1699	99.5	2130	US-09-740-369-1	Sequence 1, Appl
5	1278.2	74.9	1707	US-08-939-309-1	Sequence 1, Appl
6	1278.2	74.9	1707	US-09-849-180-1	Sequence 1, Appl
7	1278.2	74.9	1707	US-09-356-643B-5	Sequence 5, Appl
8	1217	71.3	1467	US-08-939-309-9	Sequence 9, Appl
9	1217	71.3	1467	US-09-849-180-9	Sequence 9, Appl
10	1217	71.3	1467	US-09-356-643B-9	Sequence 9, Appl
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14	256.2	15.0	1770	US-09-356-643B-1	Sequence 1, Appl
15	225.6	13.2	1629	US-08-939-309-5	Sequence 5, Appl
16	225.6	13.2	1629	US-09-849-180-5	Sequence 5, Appl
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19	42.4	2.1	7218	US-08-232-463-14	Sequence 14, Appl
20	36.4	2.1	921	US-09-328-352-492	Sequence 492, App
21	34.2	2.0	55216	US-09-716-865-7	Sequence 7, Appl
22	34.2	2.0	55216	US-09-716-865-23	Sequence 23, Appl
23	34.2	2.0	1830121	US-09-557-884-1	Sequence 1, Appl
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28	34	2.0	1392	US-09-496-398-37	Sequence 37, Appl
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32	32.8	1.9	32155	US-08-311-731A-1	Sequence 1, Appl
33	32.8	1.9	4403765	US-09-103-840A-2	Sequence 2, Appl
34	32.8	1.9	4411529	US-09-103-840A-1	Sequence 1, Appl
35	32.4	1.9	98844	US-09-791-211-10	Sequence 10, Appl
36	32.2	1.9	1020	US-09-107-532A-379	Sequence 379, App
37	32.2	1.9	2358	US-09-022-983-1	Sequence 1, Appl
38	32.2	1.9	2360	US-09-480-692-10	Sequence 10, Appl
39	31.6	1.9	1948	US-09-352-990-1	Sequence 1, Appl
40	31.6	1.9	2330	US-09-120-653D-4	Sequence 4, Appl
41	31.6	1.9	3910	US-09-120-653D-1	Sequence 1, Appl
42	31.6	1.9	9639	US-09-147-208-26	Sequence 26, Appl
43	31.6	1.9	9639	US-09-550-117A-26	Sequence 26, Appl
44	31.6	1.9	9690	US-09-182-145-55	Sequence 55, Appl
45	31.6	1.9	10241	US-08-508-448C-16	Sequence 16, Appl

ALIGNMENTS

RESULT 1
US-08-939-309-3
Sequence 3, Application US/08939309
Patent No. 6423527
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Zhou, Jianhui
TITLE OF INVENTION: SHINGOSINE-1-PHOSPHATE LYASE
TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESS: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Mark J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
US-08-939-309-3
Query Match 100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
US-09-849-180-3
; Sequence 3, Application US/09849180
; Patent No. 6495359
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; GENERAL INFORMATION:
; APPLICANT: Sada, Julie D.
; Zhou, Jianhui
;
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
;
; NUMBER OF SEQUENCES: 10
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98105
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/849,180
; FILING DATE: 04-May-2001
; CLASSIFICATION: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Pepe, Jeffrey C.
; REGISTRATION NUMBER: 46,985
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REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-849-180-3

Query Match 100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 481 GTGAAGGCTTATGGAAGTTTTCATGATGAGTAAACCCCTGCATCAGATATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGGAGAAATGTGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
DB 541 CTACGCAAGATAGAGGAGAAATGTGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
QY 601 GATTCGTGTGATGTGTGACTTCTGGGGGAACAGAAAGCATCTCATGAGGCTCCAAAGCA 660
DB 601 GATTCGTGTGATGTGTGACTTCTGGGGGAACAGAAAGCATCTCATGAGGCTCCAAAGCA 660
QY 661 TGTGGGATCTGGCCCTTGTGAAGGGGATCAAAATCTCAGAAATGTGCGTCCCAAGT 720
DB 661 TGTGGGATCTGGCCCTTGTGAAGGGGATCAAAATCTCAGAAATGTGCGTCCCAAGT 720
QY 721 GCCCATGCTGATTTAAACAAGCAGCAGTACTTTGGGATGGAAGATGTGCGGGTCCCA 780
DB 721 GCCCATGCTGATTTAAACAAGCAGCAGTACTTTGGGATGGAAGATGTGCGGGTCCCA 780
QY 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGGAAGAGCTATCTCAGAGAACACT 840

DB 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGGAAGAGCTATCTCAGAGAACACT 840
QY 841 GCCATGCTGCTGTTTACCCACAGACTTTCCTCATGTGTAAATGATCTGTCCTCGAA 900
DB 841 GCCATGCTGCTGTTTACCCACAGACTTTCCTCATGTGTAAATGATCTGTCCTCGAA 900
QY 901 GTGGCCCAAGCTGGCTGTCAATACAAATACCCCTTATGTCGAGCGTGTGCGGAGGC 960
DB 901 GTGGCCCAAGCTGGCTGTCAATACAAATACCCCTTATGTCGAGCGTGTGCGGAGGC 960
QY 961 TTCTCATGCTCTTATGAGAAAGCAGAGTACCAGCTGAGCACCATTGATTTCCGG 1020
DB 961 TTCTCATGCTCTTATGAGAAAGCAGAGTACCAGCTGAGCACCATTGATTTCCGG 1020
QY 1021 GTGAAGGTGTAAACAGACTTTCAGCTGACACCCATTAAGTATGCTTATGCCCCAAAGGC 1080
DB 1021 GTGAAGGTGTAAACAGACTTTCAGCTGACACCCATTAAGTATGCTTATGCCCCAAAGGC 1080
QY 1081 TCATCATGTTGTTGATAGTGAACAGATACAGAACTATCAGTTCTTCTGATGATCA 1140
DB 1081 TCATCATGTTGTTGATAGTGAACAGATACAGAACTATCAGTTCTTCTGATGATCA 1140
QY 1141 GATTCGAGGGTGGCATCTATGCTTCCCAACCATTCGACGCTCAGCGCTGTGGCATT 1200
DB 1141 GATTCGAGGGTGGCATCTATGCTTCCCAACCATTCGACGCTCAGCGCTGTGGCATT 1200
QY 1201 AGCGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
DB 1201 AGCGCAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 AAACAGATCATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
DB 1261 AAACAGATCATCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TTTGTTTGGGAATCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
DB 1321 TTTGTTTGGGAATCCCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1381 TACGACTATCAAACTGATGACTGCTGATGAGGGTGGAACTTGAACCACTTGTCCCA 1440
DB 1381 TACGACTATCAAACTGATGACTGCTGATGAGGGTGGAACTTGAACCACTTGTCCCA 1440
QY 1441 CCCAGTATTAATTTCTGATCATTCTACAGCCCGGGAAGAGTATGATCAATTC 1500
DB 1441 CCCAGTATTAATTTCTGATCATTCTACAGCCCGGGAAGAGTATGATCAATTC 1500
QY 1501 CTAAAGGACATTCGAGATCTGTCACTCAATCATGAAGATCTTAAAGGGAAGACCA 1560
DB 1501 CTAAAGGACATTCGAGATCTGTCACTCAATCATGAAGATCTTAAAGGGAAGACCA 1560
QY 1561 GGAATGGGTGCTCATCTGATGAGTGGCCCAACAACTTTACAGAGAAATATGTTGCGAA 1620
DB 1561 GGAATGGGTGCTCATCTGATGAGTGGCCCAACAACTTTACAGAGAAATATGTTGCGAA 1620
QY 1621 TTGCTCCTGATCTTCTGAGAGTGTACAGCAGCAGTGTACAGCAGCAGCAGCAGCAG 1680
DB 1621 TTGCTCCTGATCTTCTGAGAGTGTACAGCAGCAGTGTACAGCAGCAGCAGCAGCAG 1680
QY 1681 ATGAATGTTCTCCAAACCCCACTGA 1707
DB 1681 ATGAATGTTCTCCAAACCCCACTGA 1707

RESULT 3
US-09-356-643B-7
Sequence 7, Application US/09356643B
Patent No. 659666
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR

```
FILE REFERENCE: 200116.40ZC1
: CURRENT APPLICATION NUMBER: US/09/356.643B
: CURRENT FILING DATE: 1999-07-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 7
: LENGTH: 1707
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1707)
US-09-356-643B-7

Query Match      100.0%; Score 1707; DB 4; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 ATGCTACACAGACCTCTGATGTTGAAGGCTTTGAGCCCTACTTAGACATTTTGGAA 60
DB      1 ATGCTACACAGACCTCTGATGTTGAAGGCTTTGAGCCCTACTTAGACATTTTGGAA 60
QY      61 GATATCTCCACAAAGCCCAAGATTTATTAATGAGCATTTGACCAAGATGAGCCCTGG 120
DB      61 GATATCTCCACAAAGCCCAAGATTTATTAATGAGCATTTGACCAAGATGAGCCCTGG 120
QY      121 CAGCTAATTCGATGAGAGTGTGCTGTGACCCCTGCTGATAGTCTGGGGATATGAGTTTGC 180
DB      121 CAGCTAATTCGATGAGAGTGTGCTGTGACCCCTGCTGATAGTCTGGGGATATGAGTTTGC 180
QY      181 TTCCGCGCAGAGAGTTTGTGTCAGAGTTTAAAAAGAAATGTTTAACTCACCAGAGAG 240
DB      181 TTCCGCGCAGAGAGTTTGTGTCAGAGTTTAAAAAGAAATGTTTAACTCACCAGAGAG 240
QY      241 ATGCCCATTAATTTGCTGTAAGATTCAGACAAAGTTGAACAGACCAAGATGATATTAGC 300
DB      241 ATGCCCATTAATTTGCTGTAAGATTCAGACAAAGTTGAACAGACCAAGATGATATTAGC 300
QY      301 AAGAACATGTCATTCCTGAAGAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGT 360
DB      301 AAGAACATGTCATTCCTGAAGAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGT 360
QY      361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTCATGAGAGCCCTTCTGGG 420
DB      361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTCATGAGAGCCCTTCTGGG 420
QY      421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAACTCATGAGCTCTT 480
DB      421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAACTCATGAGCTCTT 480
QY      481 GTGAAGGCTTATGAGAGATTTTGCATGAGTAACCCCTGCATCCAGATATCTTCCACAGA 540
DB      481 GTGAAGGCTTATGAGAGATTTTGCATGAGTAACCCCTGCATCCAGATATCTTCCACAGA 540
QY      541 CTAGCAAGATAGAGGCGAAATTTGAGATAGCTTCTCCCTGTTAAATGGGGAGACA 600
DB      541 CTAGCAAGATAGAGGCGAAATTTGAGATAGCTTCTCCCTGTTAAATGGGGAGACA 600
QY      601 GATTGCTGTGATGCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB      601 GATTGCTGTGATGCTGCTGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY      661 TGTGGGAGATGCGCTTTGAGAGAGGAGATCAAAACTCCAGAAATTTGGCTCCCAAGT 720
DB      661 TGTGGGAGATGCGCTTTGAGAGAGGAGATCAAAACTCCAGAAATTTGGCTCCCAAGT 720
QY      721 GCCCATGCTGATTTTAACAAGAGCCAGTTACTTTGGGATGAAGATTTGGGGTCCCA 780
DB      721 GCCCATGCTGATTTTAACAAGAGCCAGTTACTTTGGGATGAAGATTTGGGGTCCCA 780
QY      781 TTGACGAGATGATGAGAGTGTGAGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
DB      781 TTGACGAGATGATGAGAGTGTGAGGCAATGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
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QY      841 GCCATGCTGCTGTTCTACACCCACAGTTTCTCATGTTGATATGATCTGCTCCGTGA 900
DB      841 GCCATGCTGCTGTTCTACACCCACAGTTTCTCATGTTGATATGATCTGCTCCGTGA 900
QY      901 GTGGCCAAAGCTGCTGCTCAATATACCCCTTCATGCTGACAGCTTTGTGGAGGC 960
DB      901 GTGGCCAAAGCTGCTGCTCAATATACCCCTTCATGCTGACAGCTTTGTGGAGGC 960
QY      961 TTCTCATGCTGCTTATGAGAGAAAGAGATACCCACAGTACAGAGAGAGAGAGAGAG 1020
DB      961 TTCTCATGCTGCTTATGAGAGAAAGAGATACCCACAGTACAGAGAGAGAGAGAGAG 1020
QY      1021 GTAAAGGTGTAACAGCATTTTACAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
DB      1021 GTAAAGGTGTAACAGCATTTTACAGTACAGAGAGAGAGAGAGAGAGAGAGAGAG 1080
QY      1081 TCATCATTTGCTGTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
DB      1081 TCATCATTTGCTGTTATATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1140
QY      1141 GATTGCGAGGGGTGATCTATGCTTCCCAACCATCGAGGCTCAGGCTGCTGTCAT 1200
DB      1141 GATTGCGAGGGGTGATCTATGCTTCCCAACCATCGAGGCTCAGGCTGCTGTCAT 1200
QY      1201 AGCGAGCCTGTTGGGCTGCTTGTATGACATTTGAGAGAGAGAGAGAGAGAGAGAG 1260
DB      1201 AGCGAGCCTGTTGGGCTGCTTGTATGACATTTGAGAGAGAGAGAGAGAGAGAGAG 1260
QY      1261 AAGCAGATATCAAAACGCTGCTCTCTCAAGTACAGAGAGAGAGAGAGAGAGAGAG 1320
DB      1261 AAGCAGATATCAAAACGCTGCTCTCTCAAGTACAGAGAGAGAGAGAGAGAGAGAG 1320
QY      1321 TTTGTTTGGGAAATCCCAATTTGACATGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1380
DB      1321 TTTGTTTGGGAAATCCCAATTTGACATGCTGAGAGAGAGAGAGAGAGAGAGAGAG 1380
QY      1381 TACGAGATATCAAAACGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
DB      1381 TACGAGATATCAAAACGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1440
QY      1441 CCCAGTATTCATTTTGTGATACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
DB      1441 CCCAGTATTCATTTTGTGATACATTAACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1500
QY      1501 CTAAAGAGATTCGAGAAATCTGCTCAATATGAGAGAGAGAGAGAGAGAGAGAGAG 1560
DB      1501 CTAAAGAGATTCGAGAAATCTGCTCAATATGAGAGAGAGAGAGAGAGAGAGAGAG 1560
QY      1561 GGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
DB      1561 GGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY      1621 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB      1621 TTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680
QY      1681 ATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1707
DB      1681 ATGAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1707

RESULT 4
US-09-740-369-1
: Sequence 1, Application US/09740369
: Patent No. 6521437
: GENERAL INFORMATION:
: APPLICANT: DUCKWORTH, DAVID MALCOLM
: APPLICANT: GODDEN, ROBERT JAMES
: APPLICANT: TESPA, TANIA TANSON
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30034-D1
: CURRENT APPLICATION NUMBER: US/09/740.369
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OY 1621 TTGTCCTCAGCTCTTGTGGACGCTTGACACACCGACACTGTACCCAGGCGACCCAG 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1621 ATATCTCCGCTCTTGTGGACGTCCCTTATACTACGACCCGCTGACTGACGCAACAG 1680
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 1681 ATGATGTTCTCCCAAAACCCCACTGA 1707
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1681 ATGAACGGTTCTCCAAAGCCCGCTGA 1707

RESULT 6
US-09-849-180-1
: Sequence 1, Application US/09849180
: Patent No. 6495359
: GENERAL INFORMATION:
:   APPLICANT: Saba, Julie D.
:             Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
:                     POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
:                     METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
:   ADDRESSEE: Seed Intellectual Property Law Group
:   STREET: 701 Fifth Avenue, Suite 6300
:   CITY: Seattle
:   STATE: Washington
:   COUNTRY: USA
:   ZIP: 98055
: COMPUTER READABLE FORM:
:   MEDIUM TYPE: Floppy disk
:   COMPUTER: IBM PC compatible
:   OPERATING SYSTEM: PC-DOS/MS-DOS
:   SOFTWARE: PatentIn Release #1.0, Version #1.30
:   CURRENT APPLICATION DATA:
:     APPLICATION NUMBER: US/09/849,180
:     FILING DATE: 04-May-2001
:     CLASSIFICATION: <Unknown>
:   ATTORNEY/AGENT INFORMATION:
:     NAME: Pepe, Jeffrey C.
:     REGISTRATION NUMBER: 46,985
:     REFERENCE/DOCKET NUMBER: 2001116, 402
:   TELECOMMUNICATION INFORMATION:
:     TELEPHONE: (206) 622-4900
:     TELEFAX: (206) 682-6031
:   INFORMATION FOR SEQ ID NO: 1:
:     SEQUENCE CHARACTERISTICS:
:       LENGTH: 1707 base pairs
:       TYPE: nucleic acid
:       STRANDEDNESS: single
:       TOPOLOGY: linear
:   FEATURE:
:     NAME/KEY: CDS
:     LOCATION: 1..1704
:   SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-849-180-1

Query Match      74.9%: Score 1278.2; DB 4; Length 1707;
Best Local Similarity 84.3%: Pred No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

OY 1 ATGCCCTACAGACGACCTTCTGATGTGGAAGGCCCTTGAGCCCTACTTAGAGATTTTGGAA 60
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 ATGCCCGGACGACGACCTCTCAAGCTGAAGAGACTGACACCTTATTTGGAGATTTGGAA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 61 GTATACCTCCACAAAAGCCCAAGAAATTATTAATGATGACATGACCAAGATATAGCCCTGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 TCTTATTCACAAAAGCCCAAGAAATTATGAAATGATATGACACCAAAATATAGCCCTGG 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 121 CAGCTAAATGATGAGTGTGCTGTGACACCCGTGATAGTCTGGGGATATGATTTGTC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CAGCTCAATTTGGGTGAGTGTCTGTGTACTGTCTGATATGTCTGGGTGATAGCTTATC 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
OY 181 TTCCAGCCAGAGAGTTTATGCTCAAGGTTTAAAAAGAAATGTTTTTAAGCTCACCAAGAAG 240
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

[illegible]

Db 1261 AAGAGATCATCAAAAGCTGCTGCTCTCTGTAAGTCAGAACTGGAACATCAAAACATC 1320
Qy 1321 TTGCTTTTGGGAATCCCAATTCATCTGCTGCTGAGATCCGCTGATTTTGACATC 1380
Db 1321 TTCAATTTTGGGATCCCAATTCATCTGCTGCTGAGATCCGCTGATTTTGACATC 1380
Qy 1381 TACGACTATTAACCTGATGATGCTGCTGAGATGCTGAGATGCTGAGATGCTGAGAT 1440
Db 1381 TACGACTATTAACCTGATGATGCTGAGATGCTGAGATGCTGAGATGCTGAGAT 1440
Qy 1441 CCCAGTATTCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Db 1441 AGAAGCATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1500
Qy 1501 CTAAAGCATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Db 1501 CTAAAGCATTCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1560
Qy 1561 GGAATGGGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1561 GGAATGGGTCATCTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Qy 1621 TTGCTCTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Db 1621 ATATCTCTGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1680
Qy 1681 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1707
Db 1681 ATGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1707

RESULT 7
US-09-356-643B-5
: Sequence 5, Application US/09356643B
: Patent No. 6569666
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: FILE REFERENCE: 200116.402C1
: CURRENT APPLICATION NUMBER: US/09/356.643B
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1707
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1707)
: US-09-356-643B-5

Query Match 74.9%; Score 1278.2; DB 4; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

Qy 1 ATGCTAGACAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Db 1 ATGCTAGACAGACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 60
Qy 61 GTATATCTCCAAAGCAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 120
Db 61 GTATATCTCCAAAGCAAGATTAATGATGATGATGATGATGATGATGATGATGATGAT 120
Qy 121 CAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 121 CAGTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Qy 181 TTCCAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240
Db 181 TTCCAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 240

Qy 241 ATGCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Db 241 ATGCCATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 300
Qy 301 AAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Db 301 AAGAACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360
Qy 361 CTGAGCTCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Db 361 CTGAGCTCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 420
Qy 421 CAAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Db 421 CAAGAGGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 480
Qy 481 GTGAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Db 481 GTGAAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 540
Qy 541 CTAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Db 541 CTAGCAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 600
Qy 601 GATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 601 GATTCGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Qy 661 TGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Db 661 TGTGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 720
Qy 721 GCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Db 721 GCCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 780
Qy 781 TTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Db 781 TTGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
Qy 841 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 GCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 900
Qy 901 GTGACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Db 901 GTGACCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 960
Qy 961 TTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Db 961 TTCTCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
Qy 1021 GTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 GTGAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1081 TCATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 TCATCATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Qy 1141 GATTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Db 1141 GATTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1200
Qy 1201 AGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Db 1201 AGGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1260
Qy 1261 AAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320
Db 1261 AAGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1320

OY		721	GCCCATCTCGATTTAACAAAGCAGCCAGTACTCTTGSGAATGGAAGATTGGGCGGTCCA	780
Db		721	GCCCCATCTCGATTTAACAAAGCAGCCAGTACTCTTGSGAATGGAAGATTGGGCGGTCCA	780
OY		781	TTGCACGAAGATGATGAGAGTGSATGTAGGGCAATGAGAAGACTATCTCAGAACACT	840
Db		781	TTGCACGAAGATGATGAGAGTGSATGTAGGGCAATGAGAAGACTATCTCAGAACACT	840
OY		841	GCCATGCTCGTCTGTCTACCCCACAGTTTCCTCATGGTGTATAGATTCCTGTCCGAA	900
Db		841	GCCATGCTCGTCTGTCTACCCCACAGTTTCCTCATGGTGTATAGATTCCTGTCCGAA	900
OY		901	GTGGCCAAAGCTGGGTGTCAAATACAAAATACCCTTCATGTGACAGCTTGTCTGGGAGGC	960
Db		901	GTGGCCAAAGCTGGGTGTCAAATACAAAATACCCTTCATGTGACAGCTTGTCTGGGAGGC	960
OY		961	TTCCCTCATGCTTTATGAGAAAGCAGATACCCATCGAGACACCATTGTGATTTCGG	1020
Db		961	TTCCCTCATGCTTTATGAGAAAGCAGATACCCATCGAGACACCATTGTGATTTCGG	1020
OY		1021	GTGAAGGTGTAAACACGATTTACGCTGACACCCATAGATGTGGCTATGCCCAAAGGC	1080
Db		1021	GTGAAGGTGTAAACACGATTTACGCTGACACCCATAGATGTGGCTATGCCCAAAGGC	1080
OY		1081	TCAATCATTTGGTGTATAGTAGACAABAAGTACGAAAGTATCAGTTCCTGTGATACA	1140
Db		1080	-----	1059
OY		1141	GATTGAGCAGGGTGATCTATGCTTCCCAACATCGCAGAGCTCACGGCTGTGGCATT	1200
Db		1060	-----	1059
OY		1201	AGCGCAGCCGTGTGGCTGCCTTGATGACACTTCGGGTGAGAACGGCTATGTTGAAGTACC	1260
Db		1060	-----	1059
OY		1261	AAACAGATCATCAAAACGTGCTCGCTTCTCAAGTCAGACACTGGAATAATATCAAAAGCATC	1320
Db		1060	-----CTGGAATAATATCAAAAGGCATC	1080
OY		1321	TTTTGTTTTGGGAATCCCAATTGTCACTATGCTCTGGGATCCGCTGATTTTGGACATC	1380
Db		1081	TTTTGTTTTGGGAATCCCAATTGTCACTATGCTCTGGGATCCGCTGATTTTGGACATC	1140
OY		1381	TACCGACTATCAAACTGTATGCTGTAAAGGGTGGAACTTGAAACCAGTTGACAGTTCCCA	1440
Db		1141	TACCGACTATCAAACTGTATGCTGTAAAGGGTGGAACTTGAAACCAGTTGACAGTTCCCA	1200
OY		1441	CCCAATATTCATTTCTGTGATCACATTTCTACAGCCCGGAAACGATAGCATTCATTC	1500
Db		1201	CCCAATATTCATTTCTGTGATCACATTTCTACAGCCCGGAAACGATAGCATTCATTC	1260
OY		1501	CTAAAGGACATTCGAGAATCTGTCACTCAATATGAAAGATCCTAAAGCGAAGACCACA	1560
Db		1261	CTAAAGGACATTCGAGAATCTGTCACTCAATATGAAAGATCCTAAAGCGAAGACCACA	1320
OY		1561	GGAAATGGGTGCATCTATGCCATGGCCCAAGCAACTGTGACAGGAATATGTGTGCAGAA	1620
Db		1321	GGAAATGGGTGCATCTATGCCATGGCCCAAGCAACTGTGACAGGAATATGTGTGCAGAA	1380
OY		1621	TTGTGTCATGACTCTTGTGGACAGCTGTGTACAGCAGCACTGTACACCAGGAGGACGAG	1680
Db		1381	TTGTGTCATGACTCTTGTGGACAGCTGTGTACAGCAGCAGCACTGTACACCAGGAGGACGAG	1440
OY		1681	ATGAATGGTCTCCAAAAACCCCACTGA	1707
Db		1441	ATGAATGGTCTCCAAAAACCCCACTGA	1467

	; Patent No.6569666					
	; GENERAL INFORMATION:					
	; APPLICANT: Saba, Julie D.					
	; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,					
	; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND					
	; FILE REFERENCE: 200116.40ZC1					
	; CURRENT APPLICATION NUMBER: US/09/356,643B					
	; SOFTWARE: FastSeq for Windows Version 4.0					
	; SEQ ID NO 9					
	; LENGTH: 1467					
	; TYPE: DNA					
	; ORGANISM: Homo sapiens					
	; FEATURE:					
	; NAME/KEY: CDS					
	; LOCATION: (1)...(1467)					
	US-09-356-643B-9					
	Query Match 71.3%; Score 1217; DB 4; Length 1467;					
	Best Local Similarity 85.9%; Pred No. 0;					
	Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1					
Oy	1	ATGCCTACAGACACTTCGTGATGTTGAAGCCCTTGGACCCTTAGAGATTGGA	60			
Dd	1	ATGCCTACAGACACTTCGTGATGTTGAAGCCCTTGGACCCTTAGAGATTGGA	60			
Oy	61	GTAATCTCCACAAGAAGCAAAATAATGTAATGACATTTGACCAAGATAGGCCCTG	120			
Dd	61	GTAATCTCCACAAGAAGCAAAATAATGTAATGACATTTGACCAAGATAGGCCCTG	120			
Oy	121	CAGCTAATTCGATGAGAGTGCGTGTGAGACCCTGCTGATAGTCTGGGATATAGTTTGC	180			
Dd	121	CAGCTAATTCGATGAGAGTGCGTGTGAGACCCTGCTGATAGTCTGGGATATAGTTTGC	180			
Oy	181	TTCACGCCAGAGAGATTATGTCGAAGTTTTAAAAAANAATGTTTTAAGCTCACCGAAG	240			
Dd	181	TTCACGCCAGAGAGATTATGTCGAAGTTTTAAAAAANAATGTTTTAAGCTCACCGAAG	240			
Oy	241	ATGCCCATTAATGTCGTGATGATTCAGACAAAGTTGAACAAACCAAGGATGATTTAGC	300			
Dd	241	ATGCCCATTAATGTCGTGATGATTCAGACAAAGTTGAACAAACCAAGGATGATTTAGC	300			
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Dd	601	GATTCGTGTGATGTGTGACTTCTGGGGAGACAGAAAGCATATCTCATGGCTTCAGAAAGCA	660			
Oy	661	TGTGGGAGATCTGGCCCTTTGAGAAAGGGATCAAAACTCCGGAANAATTTGGCTCCCCAAGT	720			
Dd	661	TGTGGGAGATCTGGCCCTTTGAGAAAGGGATCAAAACTCCGGAANAATTTGGCTCCCCAAGT	720			
Oy	721	GCCCATGCTCATTTTACAAACACCAAGTTACTTTGGGATGAGATTGTGGGGTCCCA	780			


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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Mark J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
US-08-939-309-7

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Query Match      15.0%; Score 256.2; DB 4; Length 1770;
Best Local Similarity 55.0%; Pred. No. 1,6e-72;
Matches 592; Conservative 0; Mismatches 473; Indels 12; Gaps 4;

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DB 485 CCCAATGGAAGAGAGAGAGAGTCTGTGTCCTGCTTACACGGGTGATGATTTGATCC 544
QY 473 AGCTCTCTGGAAGCCTATGAGATTTGATGAGAGTAAACCCCTGCATCCAGATCT 532
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QY 533 TCCAGAGCTACCAAGATAGAGCAGAAATTTGAGATAGCTTGTCTCCCTGTCATG 592
DB 605 TTCTCGCCGTAAGTAAATGGAATCCGAAAGTGTCTTATGTTTAAAGATGTTATG 664
QY 593 GGGGACAGATTCGTGTGATGTGTG--ACTTCTGGGGAGACAGAAAGCATCTCATG 649
DB 665 CCCCTCTGATACAGGTGTGTGACCAACTTCAGGTGTGATACAGATCTCTGTTAG 724
QY 650 CCGTCAAGCATGTGGGATCTGGCTTTAGAA--GGGATCAAAACTCCAGAAATTG 706
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DB 1025 ACAGTTGTCTAGGTTCTTTATGTTTCAATTTAGAAAGGCTGGTTAAAAAATCTGC 1084
QY 1004 ACCCATTTGATTTCCGGGTAAAGGTAAACAGCATTTGACCTGACACCATTAAGTATG 1063
DB 1085 CATTAATTGACTTAGAGTCCCGGAGTCACTCAATATCATGTGACACTCATTAATATG 1144

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QY 1064 GCTATGCCCAAAAGGCTCATCTGTTGTTATAGTGAACAAGATACAGAACTATC 1123
DB 1145 GATTTCACCAAAAGGCTGCTAGTTATATATGATGAAGACAGCACTTACGATGATC 1204
QY 1124 AGTTCTTCGTCATACAGATTTGCAAGGTGGCATCTATGCTTCCCAACCATGCGAGCT 1183
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QY 1184 CAGGCGCTGTCATTAAGGCGAGCGCTGGGCTGCTGATGACCTTGAGGAGAAC 1243
DB 1265 CAGGCGCTGCTGATTTGCTGATGTTGTTGGCCACTATGTCACATGAGTGAATAATG 1324
QY 1244 GCTATGTTGAGCTACCAACAGATCATCAAAATGCG--TCCCTTCCTCAATCAGAAC 1300
DB 1325 GGTACATTTGAGTGTGCGCAAGAAATATGCGGTGCGACAGATGAAGTTTAAATAATACATCC 1384
QY 1301 TGAATAATATCAAGGATCTTTGTTTGGGAATCCCAATTTGTCACATGCTCTG 1360
DB 1385 AGGAAAAATTCACAGCTGAATATGATGGCAACCTAGATATTCAGTCAATTTT 1444
QY 1361 GATCCGCTGATTTGACATCTACCGACTATCAACACCTGATGACTGTAAGGGTGAAC 1420
DB 1445 CTTCAAAGACCTTGACATACAGACTATCTGACAGTTGTCCAAAGAAAGCTGGCAT 1504
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DB 1505 TCATATGCCCTACAAAGCCGTTGCACTACACATGCGCTTCACAGAGATTGAGCGCTC 1561

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RESULT 13
US-09-849-180-7
Sequence 7, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116,402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1770 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1767
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

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US-09-849-180-7

Query Match 15.0%: Score 256.2: DB 4: Length 1770:
Best Local Similarity 55.0%: Pred. No. 1.6e-72:
Matches 592: Conservative 0: Mismatches 473: Indels 12: Gaps 4:

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QY 413 CCTTCTGCGAAGGGGAGAGCCCTGTGAAACAGTGTACAGTGGGAGAGAAAGCTCACTG 472
DB 485 CCCAATGGAGAGAAAGGAGTCTGTGGTCCGTTTACCACGGTGTGATGTTGATCC 544
QY 473 AGCTCTGTGAGAGCTATGAGATTTTGCATGAGTAACCCCTGATCCAGATPATCT 532
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QY 593 GGGGACCAAGATTCGTGTGAGTGTG---ACTTCTGGGGGGAACAGAAAGCATATCTAG 649
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QY 824 CATATCCAGAAAGCTGCATGCTGCTGTCTTCAACCCAGATTTCCCTGATGATGA 883
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QY 884 TAGATCTGTCTCCCTGAAGTGGCAAGCTGTGCTCAATATCAAAATACCCCTTCATGTCG 943
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RESULT 14

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US-09-356-643B-1
; Sequence 1, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 2001.6.40ZC1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1770
; TYPE: DNA
; ORGANISM: S. cerevisiae
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1770)
US-09-356-643B-1
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Query Match 15.0%: Score 256.2: DB 4: Length 1770:
Best Local Similarity 55.0%: Pred. No. 1.6e-72:
Matches 592: Conservative 0: Mismatches 473: Indels 12: Gaps 4:

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QY 413 CCTTCTGCGAAGGGGAGAGCCCTGTGAAACAGTGTACAGTGGGAGAGAAAGCTCACTG 472
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Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 10:43:02 : Search time 436 Seconds
(without alignments)
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Perfect score: 1707
Sequence: 1 atgcctagcacacacctctc.....gtctccaaccaccacatga 1707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1708419 seqs, 1275431651 residues

Total number of hits satisfying chosen parameters: 3416838

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Database : Published_Applications_NA.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	1707	12	US-10-197-073-3
2	1707	100.0	1707	12	US-10-053-510-7
3	1707	100.0	1707	14	US-10-286-175-3
4	1702.2	99.7	1707	12	US-10-053-510-17
5	1699	99.5	2130	10	US-09-740-369-1
6	1699	99.5	5741	11	US-09-967-668-3
7	1278.2	74.9	1707	12	US-10-197-073-1
8	1278.2	74.9	1707	12	US-10-053-510-5
9	1278.2	74.9	1707	14	US-10-286-175-1
10	1217	71.3	1467	12	US-10-197-073-9
11	1217	71.3	1467	12	US-10-053-510-9
12	1217	71.3	1467	14	US-10-286-175-9
13	558	32.7	670	11	US-09-967-668-12
14	398.4	23.3	1638	12	US-10-053-510-15
15	364.8	21.4	474	11	US-09-967-669-11
16	284.4	16.7	785	10	US-09-740-369-3

17	256.2	15.0	1770	12	US-10-197-073-7	Sequence 7, Appl
18	256.2	15.0	1770	12	US-10-053-510-1	Sequence 1, Appl
19	256.2	15.0	1770	14	US-10-286-175-7	Sequence 7, Appl
20	241	14.1	54945	11	US-09-967-669-10	Sequence 10, Appl
21	225.6	13.2	1629	12	US-10-197-073-5	Sequence 5, Appl
22	225.6	13.2	1629	12	US-10-053-510-3	Sequence 3, Appl
23	225.6	13.2	1629	14	US-10-286-175-5	Sequence 5, Appl
24	80.2	4.7	3162	12	US-10-053-510-12	Sequence 12, Appl
25	68.4	4.0	243	9	US-09-923-876-202	Sequence 202, App
26	58.4	3.4	60	12	US-09-908-975-9862	Sequence 9862, Ap
27	38.6	2.3	1049	12	US-10-140-472-358	Sequence 358, App
28	38.6	2.3	1049	12	US-10-141-761-358	Sequence 358, App
29	38.6	2.3	1049	12	US-10-142-885-358	Sequence 358, App
30	38.6	2.3	1049	12	US-10-158-780-358	Sequence 358, App
31	38.6	2.3	1049	12	US-10-123-155-358	Sequence 358, App
32	38.6	2.3	1049	15	US-10-146-644-312	Sequence 358, App
33	38.2	2.2	802	14	US-10-184-644-312	Sequence 312, App
34	38.2	2.2	802	14	US-10-184-634-312	Sequence 312, App
35	37.8	2.2	3576	14	US-10-189-971-17	Sequence 17, Appl
36	37.8	2.2	3621	14	US-10-189-971-19	Sequence 19, Appl
37	37.8	2.2	4431	14	US-10-189-971-7	Sequence 7, Appl
38	37.8	2.2	4605	14	US-10-189-971-13	Sequence 13, Appl
39	37.8	2.2	4779	14	US-10-189-971-3	Sequence 3, Appl
40	37.6	2.2	1268	8	US-08-781-986A-293	Sequence 293, App
41	36.4	2.1	1056	13	US-10-027-633-30930	Sequence 30930, A
42	36.2	2.1	2277	14	US-10-189-971-21	Sequence 21, Appl
43	36.2	2.1	3753	14	US-10-189-971-5	Sequence 5, Appl
44	36.2	2.1	3753	14	US-10-189-971-15	Sequence 15, Appl
45	36.2	2.1	4026	14	US-10-189-971-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
US-10-197-073-3
Sequence 3, Application US/10197073
Publication No. US20030166897A1

GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197,073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvater, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116.40202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ. ID NO. 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 3
US-10-197-073-3

Query Match 100.0%; Score 1707; DB 12; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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301 AAGAACATGTCTATTTCTGTAAGAGTGAACAAGATGTAAGAAAGCTTTTACCTCCAGAGGT 360
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361 CTGACCTATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTATGAGAGCCCTTCTGG 420
361 CTGACCTATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTATGAGAGCCCTTCTGG 420
421 CAAGAGGGGAGAGCCCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTAGCTCTT 480
421 CAAGAGGGGAGAGCCCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTAGCTCTT 480
481 GTGAAGGCTTATGAGAGATTTTGCATGAGATTAACCCCTGCATCCGATATCTTCCAGAGA 540
481 GTGAAGGCTTATGAGAGATTTTGCATGAGATTAACCCCTGCATCCGATATCTTCCAGAGA 540
541 CTACCAAGATGAGAGCAAAATTTGAGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
541 CTACCAAGATGAGAGCAAAATTTGAGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
601 GATTGCTGTGATGTGTGATCTTGTGGGGAGACAGAAACATACTGATGGCCCTGCAAAACA 660
601 GATTGCTGTGATGTGTGATCTTGTGGGGAGACAGAAACATACTGATGGCCCTGCAAAACA 660
661 TGTGCGGATCTGCGCTTTGAGAGAGGGATCAAAACCTCCAGAAATTTGTGCTCCCAAGGT 720
661 TGTGCGGATCTGCGCTTTGAGAGAGGGATCAAAACCTCCAGAAATTTGTGCTCCCAAGGT 720
721 GCCCATGCTGCTTTTAAACAAAGCAGCAGTTACTTGGGATGAAGATTTGTGGGGTCCCA 780
721 GCCCATGCTGCTTTTAAACAAAGCAGCAGTTACTTGGGATGAAGATTTGTGGGGTCCCA 780
781 TTGACGAAGATGATGAGAGTGTGAGGGCAATGAGAGAGCTATCTCCAGAGAACT 840
781 TTGACGAAGATGATGAGAGTGTGAGGGCAATGAGAGAGCTATCTCCAGAGAACT 840
841 GCCATGCTGCTGCTTTTACCCACAGATTTCTCATGTGTAATGATCTGCTCCCTGAA 900
841 GCCATGCTGCTGCTTTTACCCACAGATTTCTCATGTGTAATGATCTGCTCCCTGAA 900
901 GTGGCAGAGCTGGCTGTCAAAATACAAATACCCCTCATGTGAGAGCTGTGCTGGAGGC 960
901 GTGGCAGAGCTGGCTGTCAAAATACAAATACCCCTCATGTGAGAGCTGTGCTGGAGGC 960

901 GTGGCAGAGCTGGCTGTCAAAATACAAATACCCCTCATGTGAGAGCTGTGCTGGAGGC 960
961 TTCTCATGCTCTTTATGAGAGAAAGCAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
961 TTCTCATGCTCTTTATGAGAGAAAGCAGAGATACCCACTGAGAGACCATTTGATTTCCGG 1020
1021 GTGAAGGTGTACAGAGCTTTTACAGTACACCCCTTAAGTATGCTATGCCCCAAAGGC 1080
1021 GTGAAGGTGTACAGAGCTTTTACAGTACACCCCTTAAGTATGCTATGCCCCAAAGGC 1080
1081 TCATCATGCTGCTTTATGAGAGAAAGTACAGAGATACCTTCTGCTGATGACA 1140
1081 TCATCATGCTGCTTTATGAGAGAAAGTACAGAGATACCTTCTGCTGATGACA 1140
1141 GATTGGCAGAGGTGGCATGTATGCTTCCCAACATGCGAGGCTCAGGCTGTGGCATTT 1200
1141 GATTGGCAGAGGTGGCATGTATGCTTCCCAACATGCGAGGCTCAGGCTGTGGCATTT 1200
1201 AGCGCAGCCTGTTGGGCTGCTGTGATGACATTCGGTGAAGAGGCTATGTTGAAGCTACC 1260
1201 AGCGCAGCCTGTTGGGCTGCTGTGATGACATTCGGTGAAGAGGCTATGTTGAAGCTACC 1260
1261 AAACAGATCATCAAAACAGTGTGCTGCTGCAAGTGAAGAGTGAAGAAATATCAAAAGCATTC 1320
1261 AAACAGATCATCAAAACAGTGTGCTGCTGCAAGTGAAGAGTGAAGAAATATCAAAAGCATTC 1320
1321 TTTGTTTGGGAAATCCCAATTTGCTACATGCTCTGAGATCCCGTGAATTTTGACATTC 1380
1321 TTTGTTTGGGAAATCCCAATTTGCTACATGCTCTGAGATCCCGTGAATTTTGACATTC 1380
1381 TACGACATCATCAAAACCTGATGATGCTTAAGGGGTGGAACCTTGAACCAATTTGACATTC 1440
1381 TACGACATCATCAAAACCTGATGATGCTTAAGGGGTGGAACCTTGAACCAATTTGACATTC 1440
1441 CCCGATTTATCTTCTGATCATGATTTACACAGCCCGGAAACAGAGTATACATTTTC 1500
1441 CCCGATTTATCTTCTGATCATGATTTACACAGCCCGGAAACAGAGTATACATTTTC 1500
1501 CTAAAGGACATTCGAAATCTGTCACTCAATCATGAAGATCTTAAAGGACAGACACA 1560
1501 CTAAAGGACATTCGAAATCTGTCACTCAATCATGAAGATCTTAAAGGACAGACACA 1560
1561 GGAATGGGTGCTATGATGATGAGCCAGACACATGTTGACAGAGATATGTTGACAGAA 1620
1561 GGAATGGGTGCTATGATGATGAGCCAGACACATGTTGACAGAGATATGTTGACAGAA 1620
1621 TTGCTCCTAGCTTTTGTGAGACAGCTTGTACAGACCTGTACACAGGACGACACTGTACCCAGGACGACAG 1680
1621 TTGCTCCTAGCTTTTGTGAGACAGCTTGTACAGACCTGTACAGACGACGACACTGTACCCAGGACGACAG 1680
1681 ATGAATGGTCTCCAAAACCCCACTGA 1707
1681 ATGAATGGTCTCCAAAACCCCACTGA 1707

RESULT 2
US-10-053-510-7
; Sequence 7, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Rysst, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.40ZC2
; CURRENT APPLICATION NUMBER: US/10/053.510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 1707
; TYPE: DNA

ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)...(1707)
 US-10-053-510-7

Query Match 100.0%; Score 1707; DB 12; Length 1707;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGCTTGCACACACCTTCTGATGTGAAGCCCTTTAGACCCCTACTTAGAGATTTTGAA 60
DB 1 ATGCTTGCACACACCTTCTGATGTGAAGCCCTTTAGACCCCTACTTAGAGATTTTGAA 60
QY 61 GTATCTCCACAAAAGCCCAAGATTTATGAATGACATGACCAAGATGAGCCCTGG 120
DB 61 GTATCTCCACAAAAGCCCAAGATTTATGAATGACATGACCAAGATGAGCCCTGG 120
QY 121 CAGCTAATTCATGAGTGTCTGTGAGCCCTGCTGATAGCTGGGATATGAGTTTGC 180
DB 121 CAGCTAATTCATGAGTGTCTGTGAGCCCTGCTGATAGCTGGGATATGAGTTTGC 180
QY 181 TTCCAGCCACAGAGTATATGCTCAAGTTTAAAAAGAAATGTTTAAAGCTCACCAGAG 240
DB 181 TTCCAGCCACAGAGTATATGCTCAAGTTTAAAAAGAAATGTTTAAAGCTCACCAGAG 240
QY 241 ATGCCCCATTAATGTCGTAAGATTCAGACAAAGTTGAACAAGACCAAGATGATATAGC 300
DB 241 ATGCCCCATTAATGTCGTAAGATTCAGACAAAGTTGAACAAGACCAAGATGATATAGC 300
QY 301 AAGAACATGTCATTCCTGAAAAGTGACAAAGATATGTGAAGCTTACCCTCCAGAGGT 360
DB 301 AAGAACATGTCATTCCTGAAAAGTGACAAAGATATGTGAAGCTTACCCTCCAGAGGT 360
QY 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATGACAGCTATAGAGCCCTTCTGG 420
DB 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATGACAGCTATAGAGCCCTTCTGG 420
QY 421 CAAGAGGGAGAGCCCTTGAACAGTGTACAGTGGGAGAGAGAGTCACTGAGCTCCTT 480
DB 421 CAAGAGGGAGAGCCCTTGAACAGTGTACAGTGGGAGAGAGAGTCACTGAGCTCCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCCAGATATCTTCCAGGA 540
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCCAGATATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGGCAAAATTTGACGATAGCTTTCCTGTTCAATGGGGACCA 600
DB 541 CTACGCAAGATAGAGGCAAAATTTGACGATAGCTTTCCTGTTCAATGGGGACCA 600
QY 601 GATTGCTGTGATGTGACTTCTGGGGGAACAGAAAGCATATCATGAGCCCTGCAAGCA 660
DB 601 GATTGCTGTGATGTGACTTCTGGGGGAACAGAAAGCATATCATGAGCCCTGCAAGCA 660
QY 661 TGTGGGATCTGGCCTTTGAGAAAGGGGATCAAAAATCTCAGAAATTTGTGCTCCCAAGT 720
DB 661 TGTGGGATCTGGCCTTTGAGAAAGGGGATCAAAAATCTCAGAAATTTGTGCTCCCAAGT 720
QY 721 GCCCATCTGCTTAAACAAAGCAGCACTTCTTGGGATGAAGATTTGTGGGCTCCA 780
DB 721 GCCCATCTGCTTAAACAAAGCAGCACTTCTTGGGATGAAGATTTGTGGGCTCCA 780
QY 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGAGAAGAGTATCTCCAGAACACT 840
DB 781 TTGACGAAGATGATGAGGTGATGTGAGGGCAATGAGAAGAGTATCTCCAGAACACT 840
QY 841 GCCATGCTGCTGTGTTTACCCACAGATTTCTCATGATGATATAGATCTGTCCTGAA 900
DB 841 GCCATGCTGCTGTGTTTACCCACAGATTTCTCATGATGATATAGATCTGTCCTGAA 900
QY 901 GTGGCCAAAGTGGCTGTCAAAATACAAATACCCCTTATGTCAGCGCTTGTCTGGAGGC 960
DB 901 GTGGCCAAAGTGGCTGTCAAAATACAAATACCCCTTATGTCAGCGCTTGTCTGGAGGC 960

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QY 961 TTCCATCTGCTTTATGAGAAAAGCAGATATCCACTGAGACACCCATTGATTTCCGG 1020
DB 961 TTCCATCTGCTTTATGAGAAAAGCAGATATCCACTGAGACACCCATTGATTTCCGG 1020
QY 1021 GTGAAGGTGTAAACACATTTTACGTCGACACCCATTAATGATATGCCCCAAAGCC 1080
DB 1021 GTGAAGGTGTAAACACATTTTACGTCGACACCCATTAATGATATGCCCCAAAGCC 1080
QY 1081 TCATCATTTGCTGTATGATGACAAAGATGACAGAACTATCATGTTCTTCTGTGATACA 1140
DB 1081 TCATCATTTGCTGTATGATGACAAAGATGACAGAACTATCATGTTCTTCTGTGATACA 1140
QY 1141 GATGCGAGGTGGCATCTATGCTTCCCAACCATTCACAGCTCAGCGCTGGTGGCATC 1200
DB 1141 GATGCGAGGTGGCATCTATGCTTCCCAACCATTCACAGCTCAGCGCTGGTGGCATC 1200
QY 1201 AGCGACCTGTGTGGCTGCTGTGANTGACCTTGGTGAGAAAGGCTATGTTGAAGCTACC 1260
DB 1201 AGCGACCTGTGTGGCTGCTGTGANTGACCTTGGTGAGAAAGGCTATGTTGAAGCTACC 1260
QY 1261 AATCAGATCATCAAAACTGCTCGCTTCTCAAGTCAGAACTGGAATAATCAAGGATC 1320
DB 1261 AATCAGATCATCAAAACTGCTCGCTTCTCAAGTCAGAACTGGAATAATCAAGGATC 1320
QY 1321 TTGCTTTTGGGAATCCCAATTTGTCATCTGCTGAGATCCGCTGATTTGACATC 1380
DB 1321 TTGCTTTTGGGAATCCCAATTTGTCATCTGCTGAGATCCGCTGATTTGACATC 1380
QY 1381 TACCGACTATCAAACTGATGACTGTAAAGGGTGAACTTGAACCAAGTTGCACTCCA 1440
DB 1381 TACCGACTATCAAACTGATGACTGTAAAGGGTGAACTTGAACCAAGTTGCACTCCA 1440
QY 1441 CCCAGTATTCATTTCTGATCACAATCTACTACGCCCGGGAAGAGATATCAATTC 1500
DB 1441 CCCAGTATTCATTTCTGATCACAATCTACTACGCCCGGGAAGAGATATCAATTC 1500
QY 1501 CTAAGGACATTCGAGATCTGTCTACATCAATCTGAAGAATCTTAAGGCAAGACCA 1560
DB 1501 CTAAGGACATTCGAGATCTGTCTACATCAATCTGAAGAATCTTAAGGCAAGACCA 1560
QY 1561 GGAATGGTGCATCTATGATGATGCGGAGGAGCACTGTGACAGGAATATGTTGAGAA 1620
DB 1561 GGAATGGTGCATCTATGATGATGCGGAGGAGCACTGTGACAGGAATATGTTGAGAA 1620
QY 1621 TTGCTCTCAGTCTTCTGAGACGTTGTACAGACCCAGCACTGTACCCAGGCGCAG 1680
DB 1621 TTGCTCTCAGTCTTCTGAGACGTTGTACAGACCCAGCACTGTACCCAGGCGCAG 1680
QY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
DB 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707

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RESULT 3
 US-10-286-175-3
 : Sequence 3, Application US/10286175
 : Publication No. US2003005922A1
 : GENERAL INFORMATION:
 : APPLICANT: Saba, Julie D.
 : Zhou, Jianhui
 : TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 : POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 : METHODS OF USE THEREFOR
 : NUMBER OF SEQUENCES: 10
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Seed Intellectual Property Law Group
 : STREET: 701 Fifth Avenue, Suite 6300
 : City: Seattle
 : STATE: Washington
 : COUNTRY: USA
 : Zip: 98055
 : COMPUTER READABLE FORM:


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RESULT 4
US-10-053-510-17
; Sequence 17, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyrist, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 1707
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1707)
; US-10-053-510-17

Query Match          99.7% Score 1702.2: DB 12: Length 1707:
Best Local Similarity 99.8% Pred. No. 0:
Matches 1704: Conservative 0: Mismatches 3: Indels 0: Gaps 0:

QY 1 ATGCGTAGCAGACGCTTCTGATGTGAAGGCCCTTTAGGCCCTACTTAGAGATTTGGAA 60
Db 1 ATGCGTAGCAGACGCTTCTGATGTGAAGGCCCTTTAGGCCCTACTTAGAGATTTGGAA 60
QY 61 GTATACTCCACAAAAGCCAAAGATTTATGTAATGACATTCGACCACCAAGTATGACCTGG 120
Db 61 GTATACTCCACAAAAGCCAAAGATTTATGTAATGACATTCGACCACCAAGTATGACCTGG 120
QY 121 CAGCTATTGCTAGTGTGCTGTGAGACCTGCTGATGATGCTGGGATATGATTTGTC 180
Db 121 CAGCTATTGCTAGTGTGCTGTGAGACCTGCTGATGATGCTGGGATATGATTTGTC 180
QY 181 TTCCAGCCAGAGAGTTTATGTCAGGTTTAAAAAGAAATGTTTAAAGCTCACCAGAGAG 240
Db 181 TTCCAGCCAGAGAGTTTATGTCAGGTTTAAAAAGAAATGTTTAAAGCTCACCAGAGAG 240
QY 241 ATGCCCCATTATTGCTGCTTAAGATTCAGACAGATTTGAACAAGACCAAGATGATATTAGC 300
Db 241 ATGCCCCATTATTGCTGCTTAAGATTCAGACAGATTTGAACAAGACCAAGATGATATTAGC 300
QY 301 AAGAACATGTCATTCCTGAAGTGGACAAAGATGATGTAAGCTTACCCTCCAGAGGT 360
Db 301 AAGAACATGTCATTCCTGAAGTGGACAAAGATGATGTAAGCTTACCCTCCAGAGGT 360
QY 361 CTGAGCTCATCTGCTGTTTTGGAGAAATTAAGGAGTACAGCTCTTATGAGAGCCCTTGG 420
Db 361 CTGAGCTCATCTGCTGTTTTGGAGAAATTAAGGAGTACAGCTCTTATGAGAGCCCTTGG 420
QY 421 CAAGAGGGAGAGAGCTTGGAGACAGTACAGTGGGAGAGAGAACTCACTGAGCTCTT 480
Db 421 CAAGAGGGAGAGAGCTTGGAGACAGTACAGTGGGAGAGAGAACTCACTGAGCTCTT 480
QY 481 GTGAAGGCTTATGAGATTTTGAATGAGTAAACCCCTGATCCAGATCTTCCAGGA 540
Db 481 GTGAAGGCTTATGAGATTTTGAATGAGTAAACCCCTGATCCAGATCTTCCAGGA 540
QY 541 CTACGCAAGATAGAGGCAAAATTTGAGAGATAGCTTTCCCTGTTCAATGGGGAGCA 600
Db 541 CTACGCAAGATAGAGGCAAAATTTGAGAGATAGCTTTCCCTGTTCAATGGGGAGCA 600
QY 601 GATTTCGTGTGATGTGTGACTTCTGGGGAGAAAGCAATGATCTCATGAGCCCTGCAAGCA 660
Db 601 GATTTCGTGTGATGTGTGACTTCTGGGGAGAAAGCAATGATCTCATGAGCCCTGCAAGCA 660
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QY 781 TTGACGAAGATGATGAGAGTGTGATGAGGGCAATGAGAGACTATCTCCAGAACACT 840
Db 781 TTGACGAAGATGATGAGAGTGTGATGAGGGCAATGAGAGACTATCTCCAGAACACT 840
QY 841 GCCATGCTGCTTTTACCCACAGTTTCCATGATGATGATGATGATGATGATGATGATGAT 900
Db 841 GCCATGCTGCTTTTACCCACAGTTTCCATGATGATGATGATGATGATGATGATGATGAT 900
QY 901 GTGGCAAGCTGCTGTCAAATACAAATACCCCTTCATGTCAGCGCTGTCTGGAGGC 960
Db 901 GTGGCAAGCTGCTGTCAAATACAAATACCCCTTCATGTCAGCGCTGTCTGGAGGC 960
QY 961 TTCCTCATGCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
Db 961 TTCCTCATGCTTTTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1020
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Db 1021 GTGAAGGTGTAAACAGATTTTACGTCAGACACCCATGATGATGATGATGATGATGATGAT 1080
QY 1081 TCATCATGCTGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
Db 1081 TCATCATGCTGCTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1140
QY 1141 GATTGGCAGAGTGCATCTATGCTTCCCAACATTCGACGCTACAGGCTGTGTGGCATTT 1200
Db 1141 GATTGGCAGAGTGCATCTATGCTTCCCAACATTCGACGCTACAGGCTGTGTGGCATTT 1200
QY 1201 AGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
Db 1201 AGCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
QY 1261 AAGCAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
Db 1261 AAGCAGATCATCAAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1320
QY 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTATTGCTCTGGATCCCGTATTTTGACATC 1380
Db 1321 TTTGTTTTTGGGAATCCCAATTTGTCACTATTGCTCTGGATCCCGTATTTTGACATC 1380
QY 1381 TACGACATCAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
Db 1381 TACGACATCAAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1440
QY 1441 CCCAGTATTCATTTCTGATCATCTATACAGCCCGGAAAGCAGTATGATCAATTC 1500
Db 1441 CCCAGTATTCATTTCTGATCATCTATACAGCCCGGAAAGCAGTATGATCAATTC 1500
QY 1501 CTTAAAGACATTCAGAGATCTGTGATCTCAATTCATGAAGATCTTAAAGGCAACACACA 1560
Db 1501 CTTAAAGACATTCAGAGATCTGTGATCTCAATTCATGAAGATCTTAAAGGCAACACACA 1560
QY 1561 GGAATGGGTGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
Db 1561 GGAATGGGTGCTATTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620
QY 1621 TTGTCTCAGTCTTCTTGGAGAGCTTGTACAGACCAAGTGTACCCAGAGGAGCAG 1680
Db 1621 TTGTCTCAGTCTTCTTGGAGAGCTTGTACAGACCAAGTGTACCCAGAGGAGCAG 1680
QY 1681 ATGAATGCTTCTCCAAAACCCCACTGA 1707
Db 1681 ATGAATGCTTCTCCAAAACCCCACTGA 1707
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RESULT 5
US-09-740-369-1
; Sequence 1, Application US/09740369
; Patent No. US20020168710A1
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034-D1
; CURRENT APPLICATION NUMBER: US/09/740,369
; CURRENT FILING DATE: 2000-12-19
; PRIOR APPLICATION NUMBER: EP 98300625.5
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: UK 9824026.0
; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 09/238,373
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 2130
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-09-740-369-1

Query Match      99.5%: Score 1699; DB 10; Length 2130;
Best Local Similarity 99.7%: Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 1 ATGCTAGACACAGACCTCTGTGATGTTGAAGGCGCTTGTGACCCCTACTAGATATTTGAA 60
DB 178 ATGCTAGACACAGACCTCTGTGATGTTGAAGGCGCTTGTGACCCCTACTAGATATTTGAA 237
OY 61 GATATCTCCACAAAGCCCAAGATTTATGTAATGGACATTTGACCAAGATATGAGCCCTGG 120
DB 238 GATATCTCCACAAAGCCCAAGATTTATGTAATGGACATTTGACCAAGATATGAGCCCTGG 297
OY 121 CAGCTAAATTCATGTGAGTGTCTGTGACCTGCTGATGTCGAGGATATGAGTTTGTG 180
DB 298 CAGCTAAATTCATGTGAGTGTCTGTGACCTGCTGATGTCGAGGATATGAGTTTGTG 357
OY 298 CAGCTAAATTCATGTGAGTGTCTGTGACCTGCTGATGTCGAGGATATGAGTTTGTG 357
DB 181 TTCACGCGCAGAGATTTATGTCGAAGTTTAAAAAGAAATGTTTAAAGCTCACACAGAG 240
OY 358 TTCACGCGCAGAGATTTATGTCGAAGTTTAAAAAGAAATGTTTAAAGCTCACACAGAG 417
DB 241 ATGCCCATTTATGTCGTAAGATTCAGACCAAGTTGAACAAGACCAAGATATATTAC 300
OY 418 ATGCCCATTTATGTCGTAAGATTCAGACCAAGTTGAACAAGACCAAGATATATTAC 477
DB 301 AAGAACATGTCATTCCTGAAAGTGACAAAGATATGAAAGCTTTACCTCCAGGGT 360
OY 478 AAGAACATGTCATTCCTGAAAGTGACAAAGATATGAAAGCTTTACCTCCAGGGT 537
DB 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAAGATACAGCTCTATGAGCGCTTCTG 420
OY 538 CTGAGCTCATCTGCTGTTTGGAGAACTTAAAGATACAGCTCTATGAGCGCTTCTG 597
DB 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGTCTACTGAGCTCTT 480
OY 598 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGTCTACTGAGCTCTT 657
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGAGTAAACCCCTGCATCCAGATATCTTCCAGGA 540
OY 658 GTGAAGGCTTATGAGATTTTGCATGAGAGTAAACCCCTGCATCCAGATATCTTCCAGGA 717
DB 541 CTACGCAAGATAGAGGACAGAAATTTGTAGAGATAGCTTTTCCCTGTTCAATGAGGAGCA 600
OY 718 CTACGCAAGATAGAGGACAGAAATTTGTAGAGATAGCTTTTCCCTGTTCAATGAGGAGCA 777
OY 601 GATTCGTGTGATGTGTGACTTCTGGGGAGACAGAAAGCATCTCATGCGCTGCAAGCA 660
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DB 778 GATTCGTGTGATGTGTGACTTCTGGGGAGACAGAAAGCATCTCATGCGCTGCAAGCA 837
OY 661 TGTGGGATCTGCGCTTTGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT 720
DB 838 TATCGGATCTGCGCTTTGAGAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT 897
OY 721 GCCATGCTGCTATTTAAACAGCAGCACTTACTTTGGAGTGAAGATTTGGCGGTCCCA 780
DB 898 GCCATGCTGCTATTTAAACAGCAGCACTTACTTTGGAGTGAAGATTTGGCGGTCCCA 957
OY 781 TTGACGAAGATATGAGGTGATGTGAGGGCAATGAGAGAGCATCTCCAGAAACT 840
DB 958 TTGACGAAGATATGAGGTGATGTGAGGGCAATGAGAGAGCATCTCCAGAAACT 1017
OY 841 GCCATGCTGCTGTTTCTTACCCACAGTTTCCATGATGTAATGATCTGCTCCGTGA 900
DB 1018 GCCATGCTGCTGTTTCTTACCCACAGTTTCCATGATGTAATGATCTGCTCCGTGA 1077
OY 901 GTGGCCAAAGCTGGCTCAAAATPACAAATACCCCTTCATGTGACGCTTGTGGAGGC 960
DB 1078 GTGGCCAAAGCTGGCTCAAAATPACAAATACCCCTTCATGTGACGCTTGTGGAGGC 1137
OY 961 TTCCCTCATGCTTTATGAGAGAGGATACCCACTGAGCAGCCATTTGATTTCCGG 1020
DB 1138 TTCCCTCATGCTTTATGAGAGAGGATACCCACTGAGCAGCCATTTGATTTCCGG 1197
OY 1021 GTGAAAGGTGTAAACGACATTTTCAGCTGACACCCATATGATAGCTATGCCCAAAAGGC 1080
DB 1198 GTGAAAGGTGTAAACGACATTTTCAGCTGACACCCATATGATAGCTATGCCCAAAAGGC 1257
OY 1081 TCATCATTTGCTTTGTATATGTAACAGAAAGTACAGAACTATACGTTCTTCTCATACA 1140
DB 1258 TCATCATTTGCTTTGTATATGTAACAGAAAGTACAGAACTATACGTTCTTCTCATACA 1317
OY 1141 GATTTGGCAGGTTGGATCATCTTCCCAACATGCGAGGTCACGGCTGCTGGTCATT 1200
DB 1318 GATTTGGCAGGTTGGATCATCTTCCCAACATGCGAGGTCACGGCTGCTGGTCATT 1377
OY 1201 AGCGAGCCTGTTGGGCTCTCTTATGTCATCTTGGTGAAGAGCGCTATGTAAGCTTAC 1260
DB 1378 AGCGAGCCTGTTGGGCTCTCTTATGTCATCTTGGTGAAGAGCGCTATGTAAGCTTAC 1437
OY 1261 AAACAGATCATCAAACTGCTGCTTCTCAAGTCAAGAACTGGAATATCAAAAGGCATC 1320
DB 1438 AAACAGATCATCAAACTGCTGCTTCTCAAGTCAAGAACTGGAATATCAAAAGGCATC 1497
OY 1321 TTTGTTTTGGGAATCCCAATTTGTCATCTTGGTCTGGGATCCCGTATTTTGACATC 1380
DB 1498 TTTGTTTTGGGAATCCCAATTTGTCATCTTGGTCTGGGATCCCGTATTTTGACATC 1557
OY 1381 TACCGACTATCAAACTGATGACTGTAAGGGGTGAACCTGTAACAGTTGCAAGTTCCCA 1440
DB 1558 TACCGACTATCAAACTGATGACTGTAAGGGGTGAACCTGTAACAGTTGCAAGTTCCCA 1617
OY 1441 CCCAGTATTCATTTTGTGACATACATTTACTACAGCCCGGAAACGATAGCTATACATTC 1500
DB 1618 CCCAGTATTCATTTTGTGACATACATTTACTACAGCCCGGAAACGATAGCTATACATTC 1677
OY 1501 CTAAAGGACATTCGAAATCTGCACTCAAAATCATGAAGAAATCTTAAACGGAAGACACA 1560
DB 1678 CTAAAGGACATTCGAAATCTGCACTCAAAATCATGAAGAAATCTTAAACGGAAGACACA 1737
OY 1561 GGAATGGGTGCCATCTATGCCATGGCCAGACAACTGTTGACAGGAATATGTTGACAGA 1620
DB 1738 GGAATGGGTGCCATCTATGCCATGGCCAGACAACTGTTGACAGGAATATGTTGACAGA 1797
OY 1621 TTTGCTCAGCTCTTCTTGAGACAGCTTGTACACACCGACAGCTGTACCCAGGCAAGCCAG 1680
DB 1798 TTTGCTCAGCTCTTCTTGGACAGCTTGTACACACCGACAGCTGTACCCAGGCAAGCCAG 1857
OY 1681 ATGAATGTTCTTCCAAACCCACATGA 1707
DB 1858 ATGAATGTTCTTCCAAACCCACATGA 1884
|||||
```


RESULT 6

```

US-09-967-669-3
: Sequence 3, Application US/09967669
: Publication No. US20030092650A1
: GENERAL INFORMATION:
: APPLICANT: C. Frank Bennett
: APPLICANT: Susan M. Freier
: TITLE OF INVENTION: ANTISENSE MODULATION OF SPHINGOSINE-1-PHOSPHATE LYASE EXPRESSION
: FILE REFERENCE: RTS-0259
: CURRENT APPLICATION NUMBER: US/09/967,669
: CURRENT FILING DATE: 2001-09-28
: NUMBER OF SEQ ID NOS: 90
: SEQ ID NO 3
: LENGTH: 5741
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
US-09-967-669-3

```

Query Match	99.58;	Score 1699;	DB 11;	Length 5741;
Best Local Similarity	99.78;	Pred. NO. 0;		
Matches 1702; Conservative,	0;	Mismatches 5;	Indels 0;	Gaps 0;

Oy	1	ATGCCCTACACAGACCTCTGATGTGTGGAAGGCCCTTGAGGCCCTACTTACAGATTTTGGAA	60
Db	201	ATGCCCTACACAGACCTTCTGATGTGTGGAAGGCCCTTGAGGCCCTACTTACAGATTTTGGAA	260
Oy	61	GTATATCTCACAAAAGCCAGAAATTTATGTAAATGAGCATGTGACCAAGATATGAGCCCTG	120
Db	261	GTATATCTCACAAAAGCCAGAAATTTATGTAAATGAGCATGTGACCAAGATATGAGCCCTG	320
Oy	121	CAGCAATTTGCATGGAGTGTGCTGTGGAGCCCTGATGTGTGTGGGATATATGATTTTGC	180
Db	321	CAGCAATTTGCATGGAGTGTGCTGTGGAGCCCTGATGTGTGTGGGATATATGATTTTGC	380
Oy	181	TTCCAGCCAGAGATTTTATGTGTCAAGGTTTAAAAAGAAATGTTTTAACTCCACAGAGAG	240
Db	381	TTCCAGCCAGAGATTTTATGTGTCAAGGTTTAAAAAGAAATGTTTTAACTCCACAGAGAG	440
Oy	241	ATGCCCATTTATTTGGTCTGTAAAGTTTCAAGCAAGTGTGAACAAAGCAAGATATTTAGC	300
Db	441	ATGCCCATTTATTTGGTCTGTAAAGTTTCAAGCAAGTGTGAACAAAGCAAGATATTTAGC	500
Oy	301	AAGAACATGTCAATTTCTGTAAGTGAGACAAGAGATATGTGAAGCTTTAGCCCTCCAGGGT	360
Db	501	AAGAACATGTCAATTTCTGTAAGTGAGACAAGAGATATGTGAAGCTTTAGCCCTCCAGGGT	560
Oy	361	CTGAGCTCATCTGCTGTGTTTTGGAGAACTTAAAGAGTACAGCTCTATGCAAGCCTTCTGG	420
Db	561	CTGAGCTCATCTGCTGTGTTTTGGAGAACTTAAAGAGTACAGCTCTATGCAAGCCTTCTGG	620
Oy	421	CAAGAGGGAGAGACCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTGAGCTCTT	480
Db	621	CAAGAGGGAGAGACCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTGAGCTCTT	680
Oy	481	GTGAAGGCTTATGAGATTTTTCATGTAGAGTAACCCCTGTCATCCAGATATCTTCCAGGA	540
Db	681	GTGAAGGCTTATGAGATTTTTCATGTAGAGTAACCCCTGTCATCCAGATATCTTCCAGGA	740
Oy	541	CTAGCAAGATGAGAGCAAGAAATTTGTAGAGATAGCTTGTTCCTGTTCAAATGGGGAGCA	600
Db	741	CTAGCAAGATGAGAGCAAGAAATTTGTAGAGATAGCTTGTTCCTGTTCAAATGGGGAGCA	800
Oy	601	GATTGCTGTGATGTGTGACTTCTGGGGAGACAGAAAGCATATCTCATGTGCTCCAAAGCA	660
Db	801	GATTGCTGTGATGTGTGACTTCTGGGGAGACAGAAAGCATATCTCATGTGCTCCAAAGCA	860
Oy	661	TGTGGGAGATCTGGCCTTTGAGAAAGGGAGTCAAAATCTCCAGAAATTTGTGCTCCCAAAGT	720
Db	861	TATCGGAGATCTGGCCTTTGAGAAAGGGAGTCAAAATCTCCAGAAATTTGTGCTCCCAAAGT	920

OY	721	GGCCATCGTCAATTTAACAAAGCAGCCAGTACTCTTGGAGTGAAGATTTGGCGGGTCCCA	780
Db	921	GCCCATCGTGCATTTAACAAAGCAGCCAGTACTCTTGGAGTGAAGATTTGGCGGGTCCCA	980
OY	781	TTGACGAAGATGATGAGAGGTGAGTGAAGGGCAATGAGAAGACCTATCTCCAGAACACT	840
Db	981	TTGACGAAGATGATGAGAGGTGAGTGAAGGGCAATGAGAAGACCTATCTCCAGAACACT	1040
OY	841	GCCATGCTCGTCTGTCTACCCACAGTTTCTCATGTGTAAATAGATTCCTGTCCTGAA	900
Db	1041	GCCATGCTCGTCTGTCTACCCACAGTTTCTCATGTGTAAATAGATTCCTGTCCTGAA	1100
OY	901	GTGGCGAAAGCGGGGTGTCAAATATCAAAATACCCCTTATGTCCAGCGATTCTCGGGAGGC	960
Db	1101	GTGGCGAAAGCGGGGTGTCAAATATCAAAATACCCCTTATGTCCAGCGATTCTCGGGAGGC	1160
OY	961	TTCTCATTCGTCTTATATGAGAAAGCAGAGTATCCCATGTGAGCACCATTGTGATTTCCGG	1020
Db	1161	TTCTCATTCGTCTTATATGAGAAAGCAGAGTATCCCATGTGAGCACCATTGTGATTTCCGG	1220
OY	1021	GTGAAGGTGTACCCAGCATTTTCAGCTGACACCCATTAATATGGCTATGCCCCAAAAGCC	1080
Db	1221	GTGAAGGTGTACCCAGCATTTTCAGCTGACACCCATTAATATGGCTATGCCCCAAAAGCC	1280
OY	1081	TCATCATTTGGCTGTATGATGAGAACAAAGTACAGGAACATATCATGCTTCGTGCGATACA	1140
Db	1281	TCATCATTTGGCTGTATGATGAGAACAAAGTACAGGAACATATCATGCTTCGTGCGATACA	1340
OY	1141	GATTGGCAGGGGTGCATCTATATGCTTCCCAACCATTCGACAGGCTACAGCGCTGTGGCATT	1200
Db	1341	GATTGGCAGGGGTGCATCTATATGCTTCCCAACCATTCGACAGGCTACAGCGCTGTGGCATT	1400
OY	1201	AGCGCAGCCTTGTGGGCTGCCTTATATGACACTTCGGGTGAGAACGGCTATGTTGAAGCTAAC	1260
Db	1401	AGCGCAGCCTTGTGGGCTGCCTTATATGACACTTCGGGTGAGAACGGCTATGTTGAAGCTAAC	1460
OY	1261	AAACAGATCATCAAAACGTCGCTCGCTTCCTCAAGTCAGAACCTGGAATAATATCAAAAGCATC	1320
Db	1461	AAACAGATCATCAAAACGTCGCTCGCTTCCTCAAGTCAGAACCTGGAATAATATCAAAAGCATC	1520
OY	1321	TTTGTGTTTTGGGAATCCCAATTTGTCACTCATTTGCTGGAGTCCCGTGATTTTGACATC	1380
Db	1521	TTTGTGTTTTGGGAATCCCAATTTGTCACTCATTTGCTGGAGTCCCGTGATTTTGACATC	1580
OY	1381	TACGAGCATCAAAOCGTAGTACGTGTAAGGGGTGGAACCTTGAAACGAGTTGAGATTCCCA	1440
Db	1581	TACGAGCATCAAAOCGTAGTACGTGTAAGGGGTGGAACCTTGAAACGAGTTGAGATTCCCA	1640
OY	1441	CCCAATATTCATTTCTGCATCACATTACTACACCCCGGAAACGAGTAGCTATACAAATTC	1500
Db	1641	CCCAATATTCATTTCTGCATCACATTACTACACCCCGGAAACGAGTAGCTATACAAATTC	1700
OY	1501	CTAAAGCACATTCGAGAAATCTGTACATCAATATCTGAAGAATCTCTAAAGCAGAACACACA	1560
Db	1701	CTAAAGCACATTCGAGAAATCTGTACATCAATATCTGAAGAATCTCTAAAGCAGAACACACA	1760
OY	1561	GGAATGGGTGCATCTATAGCCATGGCCACAGCAACTGTGACAGAAATATGTTGGCAGAA	1620
Db	1761	GGAATGGGTGCATCTATAGCCATGGCCACAGCAACTGTGACAGAAATATGTTGGCAGAA	1820
OY	1621	TTGTCTCAGTCTTCTTGGACAGCTGTATACAGCAGCACTGTCAACCCAGGGCAGCCAG	1680
Db	1821	TTGTCTCAGTCTTCTTGGACAGCTGTATACAGCAGCACTGTCAACCCAGGGCAGCCAG	1880
OY	1681	ATGAATGGTCTTCCAAAACCCCACTGA 1707	
Db	1881	ATGAATGGTCTTCCAAAACCCCACTGA 1907	

RESULT 7
US-10-197-073-1
; Sequence 1, Application US/10197073
; Publication No. US20030166897A1

```

GENERAL INFORMATION:
APPLICANT: Sabar, Julie D.
              Zhou, Jianhui
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvater, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116.402D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1707 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1704
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-197-073-1
Query Match      74.9% Score 1278.2; DB 12; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;
QY   1 ATGCCCTGACAGACAGCTTGTGATGTTGAAGCCCTTGAGCCCTACTTAGAGATTTGGAA    60
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    1 ATGCCCGGAAACCGACACTCTCTCAAGCTGAAGACCTTCGAGCCCTAATTTGGAGTA    60
QY   61 GTATATCTCCACAAAAGCCAGAATTTATTAATGACATTTGCACCAGATGAGCCCTGG    120
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    61 TCTTATTCACAAAAGCCAGAATAATATATGATGATGATTTGACCAAAATATGAGCCCTG    120
QY   121 CAGCTAATTCGATGAGAGTGTGCTGTGGAACCTGCTGATAGTGTGGGATATAGTTTGC    180
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    121 CAGCTCATTTGGTGTGAGAGTGTCTGTGACTGCTGATGATGCTGGGTATGAGAGCTTATC    180
QY   181 TTCCAGCCAGAGAGATTATGCTCAAGGTTTAAAAAAGAAATGTTTAAAGCTCACAGGA    240
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    181 TTCCAGCCAGAGAGATTATGCTCTCGCTTTAAAAAAAATTTAATTAAGCTTATTCAGGANG    240
QY   241 ATGCCCATTAATTTGCTGTAAGATTCACAAGACAGTTGAACAAGACCAAGAGATGATTA    300
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    241 ATGCCCATTAATTTGAGCGTAAGATGCAACACAGAGTGAGACCAAGCAAGAGATCTTGTG    300
QY   301 AAGAACAATGTCATTTCTGAAAGTGACAAAGATGTTGAAGAGCTTTACCTCCAGAGGT    360
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    301 AAGAACAATGTCATTTCTGAAAGTGACAAAGATGTTGAAGAAACCTCTCCTGCTCAGGGT    360
QY   361 CTGAGAGTCATGCTGCTTTGGAGAAATTTAAGAGTACACTGATAGAGAGCCCTTCTG    420
     ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    361 ATGGGACACAGCTGAGGTTCTGAGAGACTCAAGAGGTACACTGTCATGATGATGTTCTGG    420

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[illegible]

QY	1501	TTTAAAGGCAATCGAGAACTGTGCATCTCAATTCATGTAAGAAATCCTTAAAGCAACACACA	1560
Db	1501	CTTAAAGGATATACCGGGAACTAGTACACAAATATCTGAAGAATCCTTAAAGCTTAAGACACA <td>1560</td>	1560
QY	1561	GGAAATGGGTGCCATCTATATGCCATGGCCACAGCAACTGTGACAGGAATATGTTGCAGAA <td>1620</td>	1620
Db	1561	GGAAATGGGTGCCATCTATATGCCATGGCCACAGCAACATGACAGGAAGCTGTTGCAGAA <td>1620</td>	1620
QY	1621	TTTGTCCTCAGTCTTCTTGGACAGCTTGTACAGCACCGACACTGTACACCCAGGACGACAG <td>1680</td>	1680
Db	1621	ATATTCCTCCGCTTCTTCTTGGACTGCTTATATCTACGAGCCCGTGAAGCTCAGAGGCAACAG <td>1680</td>	1680
QY	1681	ATGAATGGTCTCCAAACCCCATG <td>1707</td>	1707
Db	1681	ATGAACGGTCTCCAAACCCCGCTGA <td>1707</td>	1707

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RESULT 8
US-10-053-510-5
: Sequence 5, Application US/10053510
: Publication No. US20030175539A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: TITLE OF INVENTION: POLYNUCLEOTIDE-1-PHOSPHATE
: TITLE OF INVENTION: POLYNUCLEOTIDES AND MOD
: FILE REFERENCE: 200116.403C2
: CURRENT APPLICATION NUMBER: US/10/053,510
: CURRENT FILING DATE: 2002-01-17
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 1707
: TYPE: DNA
: ORGANISM: Mus musculus
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (1)...(1707)
US-10-053-510-5

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Query Match	74.9%;	Score 1278.2;	DB 12;	Length 1707;
Best Local Similarity	84.3%;	Pred. No. 0;		
Matches 1439;	Conservative	0;	Mismatches 268;	Indels 0;
			Gaps	0;

[illegible]

OY	421	AAAGAGGGGAAAGCCTCTGAGAACAGTGCACGTGGGAGGAAAGCCTCAGCTACCTCTT	480
OY	421	AAAAAGGGGAAAGCCTCTGAGAGCTGTGCACATGTGGGAAACCGAAGCTCACGGACTGCTG	480
OY	481	GTGAAGGCTTATGAGATTTTTCATGTGGAGTAAACCCCTGCATATCCAGATATTTCCAGGA	540
OY	481	GTGCAAGCTTATGAGATTTTTCACGTGGAGCAATCCACTGCATATCCAGATATTTCCCTGGA	540
OY	541	CTACGCAAGATAGAGCGCAAAATTTGTGAGGATAGCTTTGTTCCCTGTTCAATGGGGACCA	600
OY	541	TTGGGGAAGTTAGAGCGCAAAATCGTTAGATGACTGTTCCTTCAATGGGGGACCA	600
OY	601	GATTCGTGTGATGTGTGACTTCTGGGGGGAACAGAAAGCATATCTCATGTGCTCGAAAGCA	660
OY	601	GATTCGTGTGATGTGTGACTTCTGGGGGGAACAGCAATCTGATGTGCTCGAAAGCT	660
OY	661	TGTGGGGATCTGGGCTTTGAGAAAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
OY	661	TACGGGACTTTGGCGTTAGAGAAAGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
OY	721	GCCCATGCTGCATTTAAACAAAGCAGCCAGTTACTTTGGGATGAAGATTTGTGCGGGTCCA	780
OY	721	GCCCATGCTGCATTTGACAAAGCAGCTCATTTATTTGGGATGAAGATTTGTGCGGGTCCA	780
OY	781	TTGACAGAAAGATGATGAGAGTGGATGTGAGGGCAATGAGAAAGCATATCTCCAGAAACCT	840
OY	781	CTGAAAAAAGCAATGAGAGTGGATGTGAGGGCAATGAAAGAGCATCTCCAGAAACCA	840
OY	841	GCCATGCTGCATCTGTTTACCCCAAGTTTCTCATGGTGTATATAGATCTGTCCCTGAA	900
OY	841	GCTATGCTGCTGTTTCTTACCCCAAGTTTCTCATGGTGTGTATGATCTGTCCCGAA	900
OY	901	GTGGCCAAAGCTGGCTGTCAATAATACAAAATACCCCTTCATGTGAGCGCTTGTCTGGAGGC	960
OY	901	GTGGCCAAAGTTAAGTGCAGATATATAATCCCACTTCATGTGAGTGTGCTGGGGGGC	960
OY	961	TTCTCATCTGCTTTATGAGAAAGCAGAGATACCCACTGAGACACCTTTGATTTCCGG	1020
OY	961	TTCTCATCTGCTTTATGAGAAAGCAGAGATACCCACTGAGAAACCAATTTGATTTCCGG	1020
OY	1021	GTGAAGGTTATACAGCAATTTCAAGCTCACACCCATAGTATGGCTATGCCCAAAAGGC	1080
OY	1021	GTGAAGGTTATACAGCAATTTCAAGCTCACAGATATCTCATAGTATGGCTATGCCCTTAAAGT	1080
OY	1081	TCATCATTTGTGTGTATAGTACAGAAAGTACAGGAATATCATGATTTCTGTGCTGATACA	1140
OY	1081	TCATCATTTGTGTGTATAGTACAGAAAGTACAGGAATATCATGATTTCTGTGCTGATACA	1140
OY	1141	GATTGGCAGGGTGGCATATATGCTTTCCCAACCATCGAGGCTCAGGGCTGTGGGCAAT	1200
OY	1141	GATTGGCAGGGTGGGCTGTACGCAATCTCCAAAGCATAGCTGTGCTCAGGGCTGTGGGCAAT	1200
OY	1201	AGCGAGAGCTGTGGGGGCTGCTTATATGACATTTGCGTGTGAAGCAGGCTATGTTGAAGCTAC	1260
OY	1201	ATTGCAAGCTTGTGGGGGCTTGTATGACATTTGCGTGTGAAGCAGGCTATGTTGAAGCTAC	1260
OY	1261	AAACAGATCATCAAAACTGTCGGTTCCTCAAGTCAGAACTGAGAAATATCAAAAGCATC	1320
OY	1261	AAACAGATCATCAAAACTGTCGGTTCCTGAAGTCAGAACTGAGAAATATCAAAAGCATC	1320
OY	1321	TTTGTGTTTGGGAATCCCAATTTGTCACTCATTTGCTGTGGGATCCCGTATTTTGACATC	1380
OY	1321	TTTGTGTTTGGGATGTCCTCAATTTGTCAATTTTGTCTGGGATCCCAAGATTTTGTGACAT	1380
OY	1381	TACGAGCATCAAAAGCTGATAGCTATAGAGGGTGAAGCAATGAAACCAATGTGCAAGTCCA	1440
OY	1381	TACGAGCATCAATATGATATGTGTGTAGAGGGTGAAGTTTATCATCTCACAGTCCA	1440
OY	1441	CCCAAGTATATTTCTGCTGACATATTTACAGCCCGGAAAGCAGTATGCTATCAATTC	1500
OY	1441	AGAAAGCATATTTCTGCTGATATAGTATGATACATATCTGGAAAGCAGTGTGCGATCCAGTTC	1500
OY	1501	CTAAAGCATATCGAATCTGTCACTCAATCATGAAGAAATCCTAAAGCAAGACCA	1560

QY	1201	GGCCAGCGCTTTGGGCGTCCGTGATGAGCACTTCGGGTGAGAAAGGGATTTGCAAGCTAC	1260
Db	1201	ATTCAGACCTTTGGGCGGCGCTTGATGCACCTTCGGTGAAGACGGCTATGTTGAAGCTACC	1260
QY	1261	AACAGATCATCAAAAAGCTCGCTTGCTCTCAAGTCAGAACTGGAAAATATCAAAAGGCATC	1320
Db	1261	AAACAGATCATCAAAAAGCTCGCTCGCTCTGAAGTCAGAACTGAAAACATCAAAAACATC	1320
QY	1321	TTTCTTTTGGGAAATCCCAATTTGCACATTCGTGCTGCGGATTCGCCGATTTTGACATC	1380
Db	1321	TTTCATTTTCGGTGATCCTCAATTTGCATTTATTTGCTCTGGGATTCACAGATTTTGCATTT	1380
QY	1381	TACCGACTATCAAAACCTGATGACTGCTAAAGGGGTGAACCTTGAAACAGTTGCAGTTGCCA	1440
Db	1381	TACCGACTATCAAAATATGATGATGCTCTAAAGGGGTGAATTTTAACTACTGCAGTTGCCA	1440
QY	1441	CCCGATATTCATTTCTGTGATCAATTACTACAGCGCCGGGAAACGAGTACTATACAAATTC	1500
Db	1441	AGAAAGCATTCATTTCTGTGATTAAGTTAGTACTACTCTGGAAACGAGTGGCGATCCAGTTC	1500
QY	1501	CTAAAGACATTCGGAATCTGTCACTGCTCAATCATGAAGAAATCTTAAAGCGAAGACACA	1560
Db	1501	CTAAAGGATATCCGGGATCAGTGCACACAAATCATGAAGAAATCTTAAAGCTAAAGCACACA	1560
QY	1561	GGAAATGGGTGCATCTATGCCATGGCCGACAACTGTTGAAGAGAAATTTGGTTGCAGAA	1620
Db	1561	GGAAATGGGTGCATCTATGGCATGGGCCGACGAACCATTTGAAGAGAAAGTGTGTGCAGAA	1620
QY	1621	TTTCTCTCAGCTCTTCTTGAGACAGCTTGTACACAGCACACACTGTCAACCCAGGGCAGCCAG	1680
Db	1621	ATATTCCTCGTCTTCTTGAGACTGCCCTTAACTACTAGGAAACCCGCTGACTAGGGCAACCCAG	1680
QY	1681	ATGAATGGTCTCTCAAAAACCCGACCTGA 1707	
Db	1681	ATGAACGGTCTCTCAAAAGCCCGGCTGA 1707	

RESULT 10
 US-10-197-073-9
 ; Sequence 9, Application US/10197073
 ; Publication No. US20030166897A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Saba, Julie D.
 ; Zhou, Jianhui
 TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98055
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/197,073
 FILING DATE: 15-Jul-2002
 CLASSIFICATION: <unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Uvater, Julie A.
 REGISTRATION NUMBER: 50,461
 REFERENCE/DOCKET NUMBER: 200116.402D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:

```

:      LENGTH: 1467 base pairs
:      TYPE: nucleic acid
:      STRANDEDNESS: single
:      TOPOLOGY: linear
:
:      FEATURE:
:      NAME/KEY: CDS
:      LOCATION: 1..1467
:      SEQUENCE DESCRIPTION: SEQ ID NO: 9
:
: OS-10-197-073-9

```

Query Match	71.3%;	Score 1217;	DB 12;	Length 1467;
Best Local Similarity	85.9%;	Pred. No. 0;		
Matches 1467; Conservative	0;	Mismatches 0;	Indels 240;	Gaps 1;

QY	1	ATGGCCATGACAGACCTTCATGATGTGAAGGCCCTTGTGGCCCTACTATGAAATTTGGAA	60
Db	1	ATGGCCATGACAGACCTTCATGATGTGAAGGCCCTTGTGGCCCTACTATGAAATTTGGAA	60
QY	61	GTATATCTCCAAAGGCCAAGATTTATGTAAATGAGACTTTCACCAACTATGAGCCCTGG	120
Db	61	GTATATCTCCAAAGGCCAAGATTTATGTAAATGAGACTTTCACCAACTATGAGCCCTGG	120
QY	121	CAGCTAATTGCGATGAGATGTCGTGTGACCCCTGCGTGAATGCTGGGGATATGAGTTGTTC	180
Db	121	CAGCTAATTGCGATGAGATGTCGTGTGACCCCTGCGTGAATGCTGGGGATATGAGTTGTTC	180
QY	181	TTCCAGCCAGAGAGTTTATGCTCAAGGTTTAAAAAGAAATGTTTTAAGCTCACAGGAAG	240
Db	181	TTCCAGCCAGAGAGTTTATGCTCAAGGTTTAAAAAGAAATGTTTTAAGCTCACAGGAAG	240
QY	241	ATGGCCAAATTATGGTCGTAAATTCAGACAGCAAGTTGAACAAGACCAGGAATGATTTATGC	300
Db	241	ATGGCCAAATTATGGTCGTAAATTCAGACAGCAAGTTGAACAAGACCAGGAATGATTTATGC	300
QY	301	AAGAACAATGTCATTTCTCTGAAGATGGACAAAGATATGTAAAGCTTTATCCCTCCAGAGGT	360
Db	301	AAGAACAATGTCATTTCTCTGAAGATGGACAAAGATATGTAAAGCTTTATCCCTCCAGAGGT	360
QY	361	CTGAGCTCATTCGCTGTTTGGAGAACTTAAGAGATACAGCTCATGAGAGCCCTTCTGG	420
Db	361	CTGAGCTCATTCGCTGTTTGGAGAACTTAAGAGATACAGCTCATGAGAGCCCTTCTGG	420
QY	421	CAAGAAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAACTCACTAGACTCTT	480
Db	421	CAAGAAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAACTCACTAGACTCTT	480
QY	481	GTGAAGGCTTATGAGATTTTGCATGTAGATAAACCCCTGCATCCAGATATCTTCCACAGA	540
Db	481	GTGAAGGCTTATGAGATTTTGCATGTAGATAAACCCCTGCATCCAGATATCTTCCACAGA	540
QY	541	CTACGCCAAGATAGAGCGCAAAATTTGTGAGATACCTTTCCTCTTAAATGGGGGACCA	600
Db	541	CTACGCCAAGATAGAGCGCAAAATTTGTGAGATACCTTTCCTCTTAAATGGGGGACCA	600
QY	601	GATTCGTGTGATGTGTACTTCTGGGGGGAACAGAAACATACATGACCTGCGCAAAACA	660
Db	601	GATTCGTGTGATGTGTACTTCTGGGGGGAACAGAAACATACATGACCTGCGCAAAACA	660
QY	661	TGTGGGGATCTGGCCCTTGGAGAAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
Db	661	TGTGGGGATCTGGCCCTTGGAGAAGGGGATCAAAACTCCAGAAATTTGTGGCTCCCAAGT	720
QY	721	GCCCATGCTGATTTAAACAAGCGCCAGTACTTGGGATGAAGATGTGGGGGTCCCA	780
Db	721	GCCCATGCTGATTTAAACAAGCGCCAGTACTTGGGATGAAGATGTGGGGGTCCCA	780
QY	781	TTTGACGAAGATGATGAGGTGATGTGAGGGCAATGAAACAGCATATCTCCAGGAACACT	840
Db	781	TTTGACGAAGATGATGAGGTGATGTGAGGGCAATGAAACAGCATATCTCCAGGAACACT	840
QY	841	GCCATGCTCGTCTGTTCTACCCACAGTTTCTCATGCTGTAATAGATCTGTCCGTGA	900
Db	841	GCCATGCTCGTCTGTTCTACCCACAGTTTCTCATGCTGTAATAGATCTGTCCGTGA	900

OY 901 GTGCCAAGCTGGCTGTCAAAATACAAAATACCCCTTCATGTGCGAGCGCTTGTGGAGGC 960
DB 901 GTGGCCAGCTGGCTGTCAAAATACAAAATACCCCTTCATGTGCGAGCGCTTGTGGAGGC 960
OY 961 TTCCATCATGCTTTATATGAGAAAGAGAGATACCCACTGTGAGACCCATTGATTTCCGG 1020
DB 961 TTCCATCATGCTTTATATGAGAAAGAGAGATACCCACTGTGAGACCCATTGATTTCCGG 1020
OY 1021 GTGAAGGCTGTACAGCATTTACGCTGACACCCCTAATGATATGCTATGCCCAAAAGGC 1080
DB 1021 GTGAAGGCTGTACAGCATTTACGCTGACACCCCTAATGATATGCTATGCCCAAAAGGC 1080
OY 1081 TCAATCATGCTGTGTATATGATGACAAAGATACAGAACTATCAGTCTTCTGCTGATACA 1140
DB 1081 ----- 1059
OY 1141 GATTGGCAGGGGTGGCATATGCTTCCCAACATCGAGGCTCAGGGCTGTGGCATTT 1200
DB 1060 ----- 1059
OY 1201 AGCGAGCGCTGTGGGCTGCTTGATGCACTTCGGTGAGAAAGGCTATGTAAGCTACC 1260
DB 1060 ----- 1059
OY 1261 AAACAGATCATCAAAACCTGCTCGCTTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1320
DB 1060 ----- 1080
OY 1321 TTTGTTTTGGGAATCCCAATTTGTCATCTCATTTGCTGGGATCCCGGATTTTGACATTC 1380
DB 1081 TTTGTTTTGGGAATCCCAATTTGTCATCTCATTTGCTGGGATCCCGGATTTTGACATTC 1380
OY 1381 TACGACATATCAAACTGTGATGCTAAGGGGTGGAACCTTGAACCACTTGCACTTGATTTCCCA 1440
DB 1441 TACGACATATCAAACTGTGATGCTAAGGGGTGGAACCTTGAACCACTTGCACTTGATTTCCCA 1440
OY 1441 CCCAGTATTCATTTCTGTGATACATTTACTACACGCCGGAACGAGTACGATATACATTC 1500
DB 1201 CCCAGTATTCATTTCTGTGATACATTTACTACACGCCGGAACGAGTACGATATACATTC 1260
OY 1501 CTAAGAGCATTCGAGATGCTGCACTCAATTCATGAAGATCCAAAGCGAAGCCACA 1560
DB 1261 CTAAGAGCATTCGAGATGCTGCACTCAATTCATGAAGATCCAAAGCGAAGCCACA 1320
OY 1561 GGAATGGTGCATCTATGATGAGCCGACCAACTGTTGACAGGAATATGTTGACAGA 1620
DB 1321 GGAATGGTGCATCTATGATGAGCCGACCAACTGTTGACAGGAATATGTTGACAGA 1380
OY 1621 TTGTCCTCAGTCTTCTGTGAGAGCTGTGACAGCAGCCGACTGTACCCAGGCGAGCCAG 1680
DB 1381 TTGTCCTCAGTCTTCTGTGAGAGCTGTGACAGCAGCCGACTGTACCCAGGCGAGCCAG 1440
OY 1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
DB 1441 ATGAATGTTCTCCAAAACCCCACTGA 1467

RESULT 11
US-10-053-510-9
; Sequence 9, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: First, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053.510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9
; LENGTH: 1467
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1467)
US-10-053-510-9
Query Match 71.3%; Score 1217; DB 12; Length 1467;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1;
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DB 1 ATGCCATACACAGACCTTCTGATGTTGAAGGCTTTGAGCCCTTACTAGATTTTGA 60
OY 61 GATATCTCCACAAAAGCCCAAGATTTATTAATGACATTTGACCAATATAGAGCCCTGG 120
DB 61 GATATCTCCACAAAAGCCCAAGATTTATTAATGACATTTGACCAATATAGAGCCCTGG 120
OY 121 CAGCTAATTTGATGAGAGTGTGCTGTGACCCCTGCTGATAGTCTGGGATATGATTTGTC 180
DB 121 CAGCTAATTTGATGAGAGTGTGCTGTGACCCCTGCTGATAGTCTGGGATATGATTTGTC 180
OY 181 TTCCAGCCAGAGATTTATGCTCAAGTTTAAAAAAGATTTTAACTACCAAGAGAG 240
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OY 241 ATGCCATATTTGTTGCTGATGATTCAGACAAAGTTGAACCAAGACCAAGATGATTTAGC 300
DB 241 ATGCCATATTTGTTGCTGATGATTCAGACAAAGTTGAACCAAGACCAAGATGATTTAGC 300
OY 301 AAGAATCATGCTATTCCTGAAAGTGACAAAGATATGTGAAGCTTTACCTCCAGGGT 360
DB 301 AAGAATCATGCTATTCCTGAAAGTGACAAAGATATGTGAAGCTTTACCTCCAGGGT 360
OY 361 CTGAGCTATCTGCTGTTTGGAGCAACTTAAGGATGACAGTCTATGAGAGCCCTTCTGG 420
DB 361 CTGAGCTATCTGCTGTTTGGAGCAACTTAAGGATGACAGTCTATGAGAGCCCTTCTGG 420
OY 421 CAAGGGGAGAGGCTCTGGAACAGTGTACAGTGGGGAGGAGAGCTGAGTCTCTT 480
DB 421 CAAGGGGAGAGGCTCTGGAACAGTGTACAGTGGGGAGGAGAGCTGAGTCTCTT 480
OY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCAATCCAGATATCTTCCACAGA 540
DB 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGCAATCCAGATATCTTCCACAGA 540
OY 541 CTAGCAAGATATGAGGCAAGAAATTTGAGATAGCTTTTCCCTGTTAAATGGGGACCA 600
DB 541 CTAGCAAGATATGAGGCAAGAAATTTGAGATAGCTTTTCCCTGTTAAATGGGGACCA 600
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DB 601 GATTGCTGTGATGTTGACTTTGAGGAGCAAGAAACATACATGCTGCAAAAGCA 660
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DB 721 GCCCATGCTGATTTTAAACAAAGCCAGCTTACTTTGGAGTGAAGATTTGTCCGCCA 780
OY 781 TTGAAGAGATGATGAGGAGTGTGAGTGTGAGGCAATGAGAAGATATCCAGGAACACT 840
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DB 841 GCAATGCTGCTGTCTTCTACCCCAAGTTTCTCATGCTGATATGATATCCCTGCTGAA 900

OY	901	TTGGCCAAGCTGGCTGTCATAATATCAAAATACCCCTTCATGTGAGCTTGTGCGGAGGC	960
Db	901	GTGGCCAAGCTGGCTGTCAATATCAAAATACCCCTTCATGTGAGCTTGTGCGGAGGC	960
OY	961	TTTCCTCATCGTCTTATGAGAGAAAGCAGAGTATCCCACTGAGACACCATTGTATTCGG	1020
Db	961	TTTCCTCATCGTCTTATGAGAGAAAGCAGAGTATCCCACTGAGACACCATTGTATTCGG	1020
OY	1021	GTGAAGGTGTAAACAGCATTTTCAGCTGACACCCATAGTATGGCTATGCCCCAAAGGC	1080
Db	1021	GTGAAGGTGTAAACAGCATTTTCAGCTGACACCCATAGTATGGCTATGCCCCAAAGGC	1080
OY	1081	TCATCATTTGGTGTATATAGTACAAAGAGTACAGAACTATCAGTCTTCCTCGCATACA	1140
Db	1081	TCATCATTTGGTGTATATAGTACAAAGAGTACAGAACTATCAGTCTTCCTCGCATACA	1140
OY	1141	GATTGGCAGGGTGCATCTATGCTTCCCAACCATGACAGCTCACGGCTGGTGGCATTT	1200
Db	1060	-----	1059
OY	1201	AGCGAGCGCTTGGGCTGCCCTTGATGCACTTCGGTGAGAACGGCTATGTTGAAGCTAAC	1260
Db	1060	-----	1059
OY	1261	AAACGATCATCAAAACCTGCTGCTTCCCTCAAGTCAAGAACTGSAAAATATCAAAAGCATC	1320
Db	1060	-----CTGSAAAATATCAAAAGCATC	1080
OY	1321	TTTGTCTTTTGGGAATCCCAATTTGTCACTCATTTGCTCTGGATCCCGTATTTTGACATC	1380
Db	1081	TTTGTCTTTTGGGAATCCCAATTTGTCACTCATTTGCTCTGGATCCCGTATTTTGACATC	1380
OY	1381	TACCGACTATCAAAACCTGATGACTGCTAAAGGGGTGGAACCTTGAACCATTTGCAGTTCCCA	1440
Db	1141	TACCGACTATCAAAACCTGATGACTGCTAAAGGGGTGGAACCTTGAACCATTTGCAGTTCCCA	1200
OY	1441	CCCAATATTCATTTTGTGATCATCATTTACACAGCCCGGAAACGAGTACTATACAAATTC	1500
Db	1201	CCCAATATTCATTTTGTGATCATCATTTACACAGCCCGGAAACGAGTACTATACAAATTC	1260
OY	1501	CTAAAGGACATTCGGAATCTGTCACTCAATCATGAATCTTAAACGGAAGACACA	1560
Db	1261	CTAAAGGACATTCGGAATCTGTCACTCAATCATGAATCTTAAACGGAAGACACA	1320
OY	1561	GGAATGGTGCATCTATGCCATGGCCAGACAACTGTTGACAGGAATATGTTGTCAGAA	1620
Db	1321	GGAATGGTGCATCTATGCCATGGCCAGACAACTGTTGACAGGAATATGTTGTCAGAA	1380
OY	1621	TTGTCTCTAGTCTTTTGGACAGCTTTGTACACAGCAGACACTGTCAACCCAGGCGACCGAG	1680
Db	1381	TTGTCTCTAGTCTTTTGGACAGCTTTGTACACAGCAGACACTGTCAACCCAGGCGACCGAG	1440
OY	1681	ATGAATGGTCTTCCAAAACCCCACTGA 1707	
Db	1441	ATGAATGGTCTTCCAAAACCCCACTGA 1467	
RESULT 12			
US-10-286-175-9			
Sequence 9, Application US/10286175			
Publication No. US20030059922A1			
GENERAL INFORMATION:			
APPLICANT: Saba, Julie D.			
Zhou, Jianhui			
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE			
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND			
METHODS OF USE THEREFOR			
NUMBER OF SEQUENCES: 10			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Seed Intellectual Property Law Group			
STREET: 701 Fifth Avenue, Suite 6300			
City: Seattle			
STATE: Washington			

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? COUNTRY: USA
? ZIP: 98055
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? BEST LOCAL SIMILARITY: 85.9%; Pred. No. 0;
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/10/286,175
? FILING DATE: 30-OCT-2002
? CLASSIFICATION: <Unknown>
? ATTORNEY/AGENT INFORMATION:
? NAME: Roseman, Steven J
? REGISTRATION NUMBER: 43,058
? REFERENCE/DOCKET NUMBER: 200116.402C3
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (206) 622-4900
? TELEFAX: (206) 682-6031
? INFORMATION FOR SEQ ID NO: 9:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1467 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1464
? SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-286-175-9
Query Match 71.3%; Score 1217; DB 14; Length 1467;
Best Local Similarity 85.9%; Pred. No. 0;
Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1
QY 1 ATGCGTACAGACAGCCCTGTGATGTGGAAAGCCCTTGAGCCCTACTTAGAGATTTTGGA 60
DB 1 ATGCCCTAGCACAGACCCTTCTGTATGTGGAAAGCCCTTGAGCCCTACTTAGAGATTTTGGA 60
QY 61 GTATACCTCCACAAAAGCCACAAGAATTATGTAAATGGACATTGCACCAAGTATGAGCCCTGG 120
DB 61 GTATCTCTCCACAAAAGCCACAAGAATTATGTAAATGGACATTGCACCAAGTATGAGCCCTGG 120
QY 121 CAGCTAATTGTCATGGAGTGTCTGTGTGGACCCCTGCTGATAGTCTGGGGATATGAGTTTGC 180
DB 121 CAGCTAATTGTCATGGAGTGTCTGTGTGGACCCCTGCTGATAGTCTGGGGATATGAGTTTGC 180
QY 181 TTCGAGCCAGAGAGTTTAATGTCGACAGGTTTAAAAAGAAATGTTTTAAGCTCCACAGAG 240
DB 181 TTCGAGCCAGAGAGTTTAATGTCGACAGGTTTAAAAAGAAATGTTTTAAGCTCCACAGAG 240
QY 241 ATGCCCATTAATTGTGTCGTAGATTCAAGACAAAGTTGAACACCAAGAGATGATTATAGC 300
DB 241 ATGCCCATTAATTGTGTCGTAGATTCAAGACAAAGTTGAACACCAAGAGATGATTATAGC 300
QY 301 AAGAATCATGTCTATTCCTCGAAGAGTGAACAAGAGTATGTGAAGCTTTACCTCCAGAGGT 360
DB 301 AAGAATCATGTCTATTCCTCGAAGAGTGAACAAGAGTATGTGAAGCTTTACCTCCAGAGGT 360
QY 361 CTGAGCTCATCTGCGTGTGTTTGGAGAAACTTAAGAGATACAGTCTATGAGAGCCCTTCTGG 420
DB 361 CTGAGCTCATCTGCGTGTGTTTGGAGAAACTTAAGAGATACAGTCTATGAGAGCCCTTCTGG 420
QY 421 CAAGAGGGGAGAGCCCTCTGGAACAGTGTACAGTGGGGAGAGAACCTCACTAGAGTCTCT 480
DB 421 CAAGAGGGGAGAGCCCTCTGGAACAGTGTACAGTGGGGAGAGAACCTCACTAGAGTCTCT 480
QY 481 GTGAAGGCTTATGAGATTTTGTGCATGAGAGTAACCCCCTGCAATCCAGATATCTTCCAGGA 540
DB 481 GTGAAGGCTTATGAGATTTTGTGCATGAGAGTAACCCCCTGCAATCCAGATATCTTCCAGGA 540
QY 541 CTAGCCAGATATGAGAGCAAGAAATTGTGAGAGTACGTTGCTGCTTCAATGSGGGAGCA 600
DB 541 CTAGCCAGATATGAGAGCAAGAAATTGTGAGAGTACGTTGCTGCTTCAATGSGGGAGCA 600

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Best Local Similarity 99.5%; Pred. No. 6.9e-111;
Matches 366; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Db 1 GTCGTAAAGATTCAAGACAAAGTTGACCAAGAGATGATATTAGCAAGACATGTCAT 60
    |||||||
OY 314 TCCTGAAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGTCTGAGCTCATCTG 373
    |||||||
Db 61 TCCTGAAGTGACAAAGAGTATGTGAAGCTTTACCCCTCCAGGGTCTGAGCTCATCTG 120
    |||||||
OY 374 CTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGAGGCTTCTGGCAAGAGGAGAG 433
    |||||||
Db 121 CTGTTTGGAGAACTTAAAGAGTACAGCTCTATGAGAGGCTTCTGGCAAGAGGAGAG 180
    |||||||
OY 434 CCTCTGSAACAGTGTACAGTGGGAGAGAAAGCTCACTGAGCTCCTTGTGAAGCTTATG 493
    |||||||
Db 181 CCTCTGSAACAGTGTACAGTGGGAGAGAAAGCTCACTGAGCTCCTTGTGAAGCTTATG 240
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OY 494 GAGATTTTGCATGAGTAACCCCTGCATCCAGATATCTTCCAGGACTACGCAAGATAG 553
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Db 241 GAGATTTTGCATGAGTAACCCCTGCATCCAGATATCTTCCAGGACTACGCAAGATAG 300
    |||||||
OY 554 AGCAGAAATTGAGAGATAGCTTGTCCCTGTTCAATGGGGAGACAGATTCTGTGAT 613
    |||||||
Db 301 AGCAGAAATTGAGAGATAGCTTGTCCCTGTTCAATGGGGAGACAGATTCTGTGAT 360
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OY 614 GTGTGACT 621
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Db 361 GTGTGACT 368
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Search completed: October 6, 2003, 13:46:51
Job time : 444 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 09:57:10 ; Search time 3744 Seconds
(without alignments)
11081.127 Million cell updates/sec

Title: US-10-053-510-7
Perfect score: 1707
Sequence: 1 atgcctagcacagactctt.....gtctccaaacccactga 1707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues
Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: em_estbda:*
2: em_esthum:*
3: em_estln:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_estl:*
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13: gb_est4:*
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15: em_estfun:*
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17: em_gss_hum:*
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20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrt:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1283	75.2	4006	11	AK037789 Mus muscu
2	1283	75.2	4008	11	AK043024 Mus muscu
3	1283	75.2	4009	11	AK036747 Mus muscu
4	1283	75.2	4030	11	AK049342 Mus muscu

Result No.	Score	Query Match	Length	ID	Description
5	1086.6	63.7	4361	11	AK030972 Mus muscu
6	693	40.6	989	13	BX353997 Mus muscu
7	671	39.3	3104	11	AK075851 Mus muscu
8	639.4	37.5	1022	10	BB610497 Mus muscu
9	619.8	36.3	976	13	BX353996 Mus muscu
10	614.2	36.0	921	13	BX353996 Mus muscu
11	591.8	34.7	809	13	BX353996 Mus muscu
12	590.2	34.6	757	13	BX353996 Mus muscu
13	588.8	34.5	739	14	CA327176 Mus muscu
14	574.6	33.7	860	14	CB202317 Mus muscu
15	558	32.7	670	9	AI701419 Mus muscu
16	551.6	32.3	734	14	CB247230 Mus muscu
17	542.8	31.8	666	10	BE467984 Mus muscu
18	535.2	31.4	715	14	CA315356 Mus muscu
19	520.2	30.5	541	10	BF514352 Mus muscu
20	516.6	30.3	594	9	AL599962 Mus muscu
21	507.4	29.7	722	13	CB525257 Mus muscu
22	506.2	29.7	511	13	BX282607 Mus muscu
23	503	29.5	843	13	BU166412 Mus muscu
24	490.2	28.7	772	14	CB249844 Mus muscu
25	486.4	28.5	746	13	BO442826 Mus muscu
26	482.8	28.3	801	10	BF787188 Mus muscu
27	482.6	28.3	766	12	BI103761 Mus muscu
28	480.2	28.1	800	14	CD348685 Mus muscu
29	475.2	27.8	963	10	BF310323 Mus muscu
30	472.6	27.7	632	13	BO769049 Mus muscu
31	472	27.7	655	12	BM663348 Mus muscu
32	470.2	27.5	979	13	BO714886 Mus muscu
33	466.8	27.3	614	13	BU701972 Mus muscu
34	458.4	26.9	614	9	AW822912 Mus muscu
35	451.4	26.4	705	12	BI105217 Mus muscu
36	449	26.3	457	9	AW651710 Mus muscu
37	448.8	26.3	541	12	BI047621 Mus muscu
38	445	26.1	545	10	BE504282 Mus muscu
39	439.6	25.8	505	10	BE152613 Mus muscu
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42	405.6	23.8	533	14	CD539780 Mus muscu
43	403.8	23.7	801	13	BU249352 Mus muscu
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ALIGNMENTS

RESULT 1
LOCUS AK037789
DEFINITION Mus musculus 16 days neonate thymus cDNA, RIKEN full-length
cDNA library, clone: A130049P18 product: sphingosine phosphate
lyase 1, full insert sequence.
ACCESSION AK037789
VERSION AK037789.1 GI:26332283
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
1 Carninci, P., Hayashizaki, Y., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL MEDLINE
PUBMED 10349636
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
10349636
Carninci, P., Hayashizaki, Y., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL MEDLINE
PUBMED 10349636
Carninci, P., Hayashizaki, Y., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL MEDLINE
PUBMED 10349636

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 Db 1096 GTGAAAGGTAAACAGCACTTTCAGCTGACACCCATAGATGAGTATGCCCCAAAGGC 1155
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 LOCUS
 DEFINITION
 Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length
 enriched library, clone:A730048M17 product:sphingosine phosphate
 lyase 1, full insert sequence.
 ACCESSION
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 VERSION
 AK043024.1 GI:26335472
 KEYWORDS
 HTC; CAP trapper.
 SOURCE
 Mus musculus (house mouse)
 ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 99279253
 MEDLINE
 PUBMED
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 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
 Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 20499374
 MEDLINE
 PUBMED
 11042159
 3
 Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P.,
 Konno, H., Akiyama, J., Nishi, K., Kusunagi, T., Tashiro, H., Itoh, M.,
 Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A.,
 Yamamoto, R., Matsumoto, H., Sakauechi, S., Ikegami, T., Kashiwagi, K.,
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 Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
 Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system-384-format
 sequencing pipeline with 384 multicapillary sequencer
 Genome Res. 10 (11), 1757-1771 (2000)
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 4
 Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
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 Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P.,
 Marchionni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P.,
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 Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, R. F., Suzuki, H.,
 Toyokawa, K., Wang, K. H., Weitz, C., Whitaker, C., Wilming, L.,
 Wyshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohsaki, S.
 and Hayashizaki, Y.
 Functional annotation of a full-length mouse cDNA collection
 Nature 409 (6821), 685-690 (2001)
 21085660
 MEDLINE

PUBMED 11217851
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 4008)
Fukuda,S., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Adachi,J., Furuno,M., Haneagaki,T., Hara,A., Hashizume,M., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiroaka,T., Hirozane,T., Horii,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishii,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakezume,N., Sano,H., Sasaki,D., Shibata,K., Shingawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suenho-cho, Tsunumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.c.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
CDNA library was prepared and sequenced in Mouse Genome Encyclopedia project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/
Location/Qualifiers
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RESULT 3
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ACCESSION AK036747
VERSION AK036747.1 GI:26331663
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ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
JOURNAL MEDLINE
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AUTHORS
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REFERENCE
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PUBMED 11042159
REFERENCE 3
AUTHORS
Shibata, K., Itoh, M., Aizawa, K., Nagaoaka, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kikunishi, T., Tashiro, H., Itoh, M.,
Sunil, I., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Matsumoto, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsunaga, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multiplexed capillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
JOURNAL MEDLINE
PUBMED 20530913
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REFERENCE 4
AUTHORS
Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y.,
Aizawa, K., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S.,
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Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R.,
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Yoshida, K., Hasegawa, Y., Kawai, H., Kohsaki, S., and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
JOURNAL MEDLINE
PUBMED 21085660
PUBMED 11217851
REFERENCE 5
AUTHORS
TITLE
The FANTOM Consortium and the RIKEN Genome Exploration Research
Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation
of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
JOURNAL MEDLINE
PUBMED 1217851
REFERENCE 6
AUTHORS
Adachi, J., Aizawa, K., Akimura, T., Arai, A., Hashizume, W.,
Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W.,
Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirokane, T.,
Hori, F., Imocani, K., Ishii, Y., Itoh, M., Kagawa, T., Kasukawa, T.,
Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,
Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M.,
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Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M., and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute; 1-7-22 Sushiro-cho, Tsukuba-shi, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES		Location/Qualifiers
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DB	859	CTGAAGAAAGACATGAGAGGTGATGTGAGGCAATGAGAAGAGCTATCTCCAGAAACACA 918
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DB	919	GCTATGCTGCTGTCTTCTACCCACAGTTTCTCATGTGTATGATGATCTCTGCTGAA 978
QY	901	GTGGCCAGAGCTGGCTGTCAAAATATACAAATACCCCTTCATGTGACAGCTTGTCTGGAGGC 960
DB	979	GTGGCCAGAGTTGGCTGTCAAGATATATAATCCACCTCATGTGTGATGCTTGTCTGGAGGC 1038
QY	961	TTCTCATGCTCTTTATGAGAAAGACAGATATCCCATGAGACACCAATTTGATTTCCGG 1020
DB	1039	TTCTCATGCTCTTTATGAGAAAGACAGATATCCCATGAGAAACCAATTTGATTTCCGG 1098
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QY	1141	GATTGGCAGGGTGCATATATGCTTCCCAACATGCGAGGCTCAGGCTCTGTGTCATT 1200
DB	1219	GACTGGCAAGGGTGTCTACGCAATCTCAAGCATAGCTGCTCAGGCTCTGTGTCATT 1278
QY	1201	AGCGACGCTGTGGGCTGCCCTGTGATGCACTTGGTGAACGGCTATGTTGAAGCTACC 1260
DB	1279	ATTGACGCTGTGGGCTGCCCTGTGATGCACTTGGTGAACGGCTATGTTGAAGCTACC 1338
QY	1261	AAACGATATCAAAACATGCTGCTCTCAAGTACAGAACTGGAATAATCAAAAGGACTC 1320
DB	1339	AAACGATATCAAAACATGCTGCTCTCAAGTACAGAACTGGAATAATCAAAAGGACTC 1398
QY	1321	TTTGTGTTTGGGAATCCCAATTTGCTACTCATTTGCTCTGGGATCCGTTGATTTGACTC 1380
DB	1399	TTTGTGTTTGGGATCCCAATTTGCTACTCATTTGCTCTGGGATCCGTTGATTTGACTC 1458
QY	1381	TACGACATCAAAACCTGATGACCTGAAGGGTGAACCTGAACCAATTCAGTGTCCCA 1440
DB	1459	TACGACATCAAAACCTGATGACCTGAAGGGTGAACCTGAACCAATTCAGTGTCCCA 1518
QY	1441	CCCATATTTCAATTTTGTGATCATTACTTACACGCGCCGAAACGAGTATACATATTC 1500
DB	1519	AGACATATTTCAATTTTGTGATCATTACTTACATCTCGAAGCAGTGTGCGATCCAGTTC 1578
QY	1501	CTAAAGACATTTGGAATCTGTCTACTCAATCATGAAGAAATCTTAAAGCAAGACACA 1560
DB	1579	CTAAAGACATTTGGAATCTGTCTACTCAATCATGAAGAAATCTTAAAGCTTAAGACACA 1638
QY	1561	GGAATGGTGCCATTTATGTCATGGCCCAAGACACTGTTGACAGGAATATGTTGTCAGAA 1620

Db 1639 GGATGCGTCCATCTATGCGATGCGCAGCAACCATGACAGGAAGCTGTTGCAGAA 1698
 Oy 1621 TTGCGCCAGCTCTTCTGAGAGCTGTACAGCACCGACACTGCACCCAGGAGCCAG 1680
 Db 1699 ATATCCCGCTCTTCTTGAGCTGCTTATCTACTAGCGACCCGCTGACTCAGGCGAACAG 1758
 Oy 1681 ATGATGTTCTCCAAAACCCACTGA 1707
 Db 1759 ATGACGCTCTCCAAAGCCCGCTGA 1785

RESULT 4
 AK049342
 LOCUS
 DEFINITION Mus musculus ES cells cDNA, RIKEN full-length enriched library, clone: C330025N24 product: sphingosine phosphatase lyase 1, full insert sequence.

ACCESSION AK049342
 VERSION AK049342.1 GI:26340063
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus

REFERENCE 1
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M., and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watabiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A., and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

TITLE
 JOURNAL
 MEDLINE
 PUBMED
 REFERENCE
 AUTHORS

JOURNAL Nature 409 (6821), 685-690 (2001)
 MEDLINE 21085660
 PUBMED 11217851
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
 JOURNAL Nature 420 563-573 (2002)
 REFERENCE 6 (bases 1 to 4030)
 AUTHORS Adachi, U., Aizawa, K., Akimura, T., Aikawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Horii, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kuribara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
 TITLE Direct Submission
 JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
 COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
 FEATURES
 source
 location/Qualifiers
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 polyA_signal
 polyA_site
 BASE COUNT 959 a 935 c 1016 g 1120 t
 ORIGIN

Query Match 75.2%; Score 1283; DB 11; Length 4030;
 Best Local Similarity 84.5%; Pred. No. 0;
 Matches 1442; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

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OY 1 ATGCTACAGACCTTCTGATGTTGAAGCCCTTGACCTACTTGAAGATTTGGAA 60
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Db 99 ATGCCGGAAACCGACTCTCTCAAGCTGAAGGACTTCGAGCTTATTTGGAGTTTGGAA 158
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OY 61 GTATACCTCCAAAGAACCAAGATATGTAATGAGCATTTGCACCAAGTATAGCCCTGG 120
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OY 181 TTCACGACAGAGATTTATGCTCAAGGTTTAAAGATTTTAAAGTCCAGAGAG 240
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OY 841 GCCATGCTGCTGTTTCAACCCAGATTTCTCATGAGTATGATATGCTCCCTCAA 900
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OY 901 GTGGCAAGCTGCTGCTCAAAATATACCCCTTCAATGTCGAGCTGTCGGAGGC 960
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Db 1119 GTGAAGAGGTATACAGAGATTTCACTGATATGATATGCTATGCTCTAAAGGT 1178
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Db 1779 ATGAAGGCTTCTCCAAACCCCACTGA 1805
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RESULT 5
 AK030972
 LOCUS 4361 bp mRNA linear HTC 05-DEC-2002
 DEFINITION Mus musculus adult male thymus cDNA, RIKEN full-length enriched library, clone:5830472016 product:splingosine phosphate lyase 1, full insert sequence.
 AK030972
 ACCESSION AK030972.1 GI:26082085
 VERSION AK030972.1
 KEYWORDS HTC; CAP trapper.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning
 Meth. Enzymol. 303, 19-44 (1999)
 JOURNAL MEDLINE 99279253
 PUBMED 10349636
 REFERENCE 2
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 Genome Res. 10 (10), 1617-1630 (2000)
 JOURNAL

[illegible]

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Db      891 GCCCATGCTCATTTGACAAAGCAGCTCTATTATTTGGATGAAATTTGGAGTTGCA 950
QY      781 TTGACGAGATGATGAGGTGATGTGAGGCAATGAGAAGCATATCTCCAGGAACCT 840
Db      951 CTGAAAAAAGACATGAGGTGATGTGACGAATGAAAGAGCCATCTCCAGGAACCA 1010
QY      841 GCCATGCTGCTGTTCTACCCACAGTTTCCATAGGTGTAATGATCTGCTCCGAA 900
Db      1011 GGTATGCTGCTGTTCTACCCACAGTTTCCATAGGTGTAATGATCTGCTCCGAA 1070
QY      901 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCATGTGACGCTGTCTGGAGGC 960
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Db      1191 GTGAAGGTGTAAACGACATTTACAGTGAACCCATTAATATGCTATGCCCAAAAGC 1250
QY      1081 TCATCATGTTGTTGATATGATGACAAGATACAGAACTATCATGTTCTTCGATACCA 1140
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Db      1311 GACTGCAAGGTGGTGTCTACCACTCTCCACATAGTGGCTCAGCGCTGGTGGCAT 1370
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Db      1371 ATTGGACCTGTTGGGCTGCTGATGACCTTCGAGAAAGCGCTATGTTGAAGTACC 1430
QY      1261 AAACAGATCATCAAAACTGCTGCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1320
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QY      1381 TACCGACTATCAAACTGATGACTGCTAGGGGTGGAACCTGAACCAAGTTGACAT 1440
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Db      1611 AGAAG 1615

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RESULT 6
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DEFINITION CDNA clone CS0DC013Y18 5-PRIME, mRNA sequence.
ACCESSION BX353997
VERSION BX353997
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 989)
AUTHORS Li, M.-Y., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Contact: Genoscope

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Genoscope - Centre National de Sequencage
BP 191 91006 Evry cedex - France
Email: seque@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5671.f. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgl-bin/cluster.cgi?seq=CS0DC013DE09Q1&cluster=5671.f. Contact :
Feng Liang Email : fliang@life.technologies.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC013DE09Q1.
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BASE COUNT 263 a 199 c 294 g 217 t 16 others.
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Best Local Similarity 97.4%; Pred. No. 7.3e-192;
Matches 698; Conservative 14; Mismatches 4; Indels 1; Gaps 1;
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DEFINITION		Mus musculus adult male stomach cDNA, RIKEN full-length enriched library, clone:2L104J4J20 product:sphingosine phosphate lyase 1, full insert sequence.
ACCESSION		AK075851
VERSION		AK075851.1 GI:26096560
KEYWORDS		HMC; CAP trapper.
SOURCE		Mus musculus (house mouse)
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE		Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA cloning Meth. Enzymol. 303, 19-44 (1999) 9279253
AUTHORS		Garcinici, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Kono, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y. Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes Genome Res. 10 (10), 1617-1630 (2000) 20499374 11042159
TITLE		Shibata, K., Itoh, M., Aizawa, K., Nagaoke, S., Sasaki, N., Carninci, P., Kono, H., Akiyama, J., Nishi, K., Kitsumagi, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazema, M., Nishino, T., Harada, A., Yamamoto, R., Matsunoto, H., Sakaguchi, S., Ikegami, T., Kasaiwaqi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohari, E., Matshiki, M., Yoneda, Y., Ishtkawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kita, A. and Hayashizaki, Y. RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000) 20530913 11076661
JOURNAL MEDLINE PUBMED REFERENCE AUTHORS		Kawai, J., Shitagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Atakawa, T., Hara, A., Fukunishi, Y., Kono, H., Adachi, J., Fukuda, S., Aizawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaoka, I., Saito, T., Okazaki, Y., Gotojori, T., Bono, H., Kesukawa, T., Saito, R., Kodote, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gaasterland, T., Giusti, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Schenckebush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washio, T., Sakai, R., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Boujinga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bolt, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Humé, D.A., Kamijima, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mommaerts, P., Nordone, P., Ring, B., Ringswald, M., Rodriguez, I., Sakamoto, N., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyok-Oka, K., Wang, K.H., Weitz, C., Whitaker, C., Wilming, L., Wynshaw-Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohzuki, S. and Hayashizaki, Y. Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001) 21085660 11217851
TITLE		The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

JOURNAL REFERENCE	AUTHORS	ANALYSIS OF THE MOUSE TRANSCRIPTOME BASED ON FUNCTIONAL ANNOTATION OF 60,770 FULL-LENGTH CDNAS
Nature 420, 563-573 (2002)	5 (bases 1 to 3104)	
Adachi, J., Aizawa, K., Hayashida, K., Hayatsu, N., Hiramoto, K., Hirooka, T., Hirozane, T., Fukuoka, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, M., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		
JOURNAL	Direct Submission	
Submitted (16-APR-2002)	Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-1-22 Suhei-cho, Tsukuba-shi, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)	
COMMENT	CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and genome science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/URL: http://genome.gsc.riken.go.jp/. location/Qualifiers	
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LOCUS BX353996 Homo sapiens NEUROBLASTOMA COR 25-NORMALIZED Homo sapiens
DEFINITION cDNA clone CS0DC013YJ18 3-PRIME, mRNA sequence.
ACCESSION BX353996
VERSION BX353996.1 GI:30371821
KEYWORDS EST
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 976)
AUTHORS Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished
COMMENT Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5671.f for
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DC013DE09NP1&cluster=5671.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :

http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC013DE09NP1.
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digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized.
BASE COUNT 265 a 199 c 239 g 260 t 13 others
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RESULT 10
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LOCUS B0846030


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DEFINITION  AGENCOURT_10413219 NIH_MGC_109 Homo sapiens cDNA clone
IMAGE:5579973 5', mRNA sequence.
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VERSION     BU846030.1 GI:24030735
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ORGANISM    Homo sapiens
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 921)
AUTHORS     NIH-MGC http://mhc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-remail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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BASE COUNT  240 a 186 c 294 g 200 t 1 others
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DEFINITION 5', mRNA sequence.
ACCESSION   BU597239
VERSION     BU597239.1 GI:23248998
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ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 809)
AUTHORS     NIH-MGC http://mhc.nci.nih.gov/.
TITLE       National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL     Unpublished
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cga@bbs-remail.nih.gov
            Tissue Procurement: NCI
            cDNA Library Preparation: Michael Brownstein Laboratory
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            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
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            Plate: L1CM2630 row: h column: 16
            High quality sequence stop: 570.
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        4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
        kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,
        ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary
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        Creator SMART kit and size-selected to contain the >0.5 kb

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size fraction (other fractions present in NIH_MGC_141).
Library created in the Laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH MGC Library."

BASE COUNT

212 a 164 c 255 g 178 t

Query Match 34.7%; Score 591.8; DB 13; Length 809;
Best Local Similarity 97.9%; Pred. No. 3.6e-162;
Matches 610; Conservative 0; Mismatches 12; Indels 1; Gaps 1;

1 ATGCTTACGACAGACCTTTGATGTGAGCCCTTTGAGCCCTTACCTAGAGATTTGGAA 60
186 ATGCTTACGACAGACCTTTGATGTGAGCCCTTTGAGCCCTTACCTAGAGATTTGGAA 245
61 GTATATCCACAAAGCCAAATTAATGATGACCTTACCAAGATATGAGCCCGG 120
246 GTATATCCACAAAGCCAAATTAATGATGACCTTACCAAGATATGAGCCCGG 305
121 CAGCTAATTCAGATGAGTGTGTCGACCTGCTGATAGTCTGGGATATGAGTTGTC 180
306 CAGCTAATTCAGATGAGTGTGTCGACCTGCTGATAGTCTGGGATATGAGTTGTC 365
181 TTCACGACAGAGATTTATGTCAGGTTTAAAAAGAAATTTTAACTCACCAGAG 240
366 TTCACGACAGAGATTTATGTCAGGTTTAAAAAGAAATTTTAACTCACCAGAG 425
241 ATGCCCATTTATTTGGTGAAGATTCAGACAAAGTTGAACAGACCAAGATATTTAGC 300
426 ATGCCCATTTATTTGGTGAAGATTCAGACAAAGTTGAACAGACCAAGATATTTAGC 485
301 AAGAATATGTCATTCCTGAAAGTGAGCAAAAGATATGTAAGCTTACCTCCAGGCT 360
486 AAGAATATGTCATTCCTGAAAGTGAGCAAAAGATATGTAAGCTTACCTCCAGGCT 545
361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACACTGATGAGAGCCTTCTGG 420
546 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACACTGATGAGAGCCTTCTGG 605
421 CAAGAGGGAGAGCCTCTGAAACAGTGTACAGTGGGAGGAGAGAGCTACTGAGCTCTT 480
606 CAAGAGGGAGAGCCTCTGAAACAGTGTACAGTGGGAGGAGAGAGCTACTGAGCTCTT 665
481 GTGAGGCTTATGAGATTTTGCATGGAACCCCTGATCCAGATATCTTCCAGCA 540
666 GTGAGGCTTATGAGATTTTGCATGGAACCCCTGATCCAGATATCTTCCAGCA 725
QY 541 CTACGCAAGATAGAGGCAAAATTTGTAGGATAGCTT-GTTCCTGTTCAATGGGGAGC 599
Db 726 CTACGCAAGATAGAGGCAAAATTTGTAGGATAGCTTGTCTCCGTTCAAGGGGGAGC 785
QY 600 AGATTGCTGTGATGTGACTT 622
Db 786 AAATTCCGGGTGATGGGGGCT 808

RESULT 12
CD348713 757 bp mRNA linear EST 29-MAY-2003
LOCUS CD348713
DEFINITION U1-M-FY0-cf8-1-11-0-U1.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6855348 5', mRNA sequence.
ACCESSION CD348713
VERSION CD348713.1 GI:31140228
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE NIH-MGC National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution Information can be found at
<http://genome.uiowa.edu/distribution/mouse1.html>
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
Seq primer: pyx-5.

FEATURES
source Location/Qualifiers

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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE: 6855348"
/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dp"
/lab_host="DH10B (T1 phage resistant)"
/clone_id="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pyx-Asc; Site:1: EcoR I;
Site:2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

BASE COUNT 193 a 170 c 190 g 203 t 1 others
ORIGIN

Query Match 34.6%; Score 590.2; DB 14; Length 757;
Best Local Similarity 86.4%; Pred. No. 1e-161;
Matches 652; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 685 GGGATCAAAATCTCCAGAAATTTGGGCTCCCAAGTGGCCATGTCATTTAACAACA 744
Db 3 GGGATCAAAATCTCCAGAAATTTGGGCTCCCAAGTGGCCATGTCATTTAACAACA 62
QY 745 GCCAGTTACTTTGGGATGAGATTTGGGGGCTCCCATTTGACGAAGATGAGGTGAT 804
Db 63 GCTCATTTATTTGGGATGAGATTTGGGGGCTCCCATTTGACGAAGATGAGGTGAT 122
QY 805 GTGAGGCAATGAGAGAGCTATGCTCCAGGAACACTGCCATGCTGCTGTTTACCCCA 864
Db 123 GTGAGGCAATGAGAGAGCTATGCTCCAGGAACACTGCCATGCTGCTGTTTACCCCA 182
QY 865 CAGTTCTCATGCTGATATGATGATCCTGCTCCGTAAGGCGCAAGCTGCTCAATAT 924
Db 183 CAGTTCTCATGCTGATGATGATCCTGCTCCGTAAGGCGCAAGCTGCTCAATAT 242
QY 925 AAATATCCCTTCATGTCGAGCTTGTCTGGAGGCTTCTTCATGCTCTTTATGAGAAA 984
Db 243 AAATATCCCTTCATGTCGAGCTTGTCTGGAGGCTTCTTCATGCTCTTTATGAGAAA 302
QY 985 GCAGGATACCCACATGAGACACCCATTTATTTCCGGGTGAAAGGTATACCAAGATTTC 1044
Db 303 GCAGGATACCCACATGAGACACCCATTTATTTCCGGGTGAAAGGTATACCAAGATTTC 362
QY 1045 GCTGACACCAATTAATGATAGTATGCTCCCAAGAGCTCATTTGCTTTATAGTGAC 1104
Db 363 GCAGATATCATTAATGATAGTATGCTCCCAAGAGCTCATTTGCTTTATAGTGAC 422
QY 1105 AAGAATGACGAATCATCACTTCTGCTGATACAGATTGGCAGAGGTGATGCTTACT 1164
Db 423 GAGAAGTACAGAGATCACTTCTGCTGATACAGATTGGCAGAGGTGATGCTTACT 482

QY 1165 TCCCAACATGCGAGGCTCAGGCGCTGGTGGCATTTAGCGACCGCTGTTGGGCTGCTTG 1224
DB 483 TCTCCAAGCATATGCTGCTCAGCGGCTGGTGGCATATTTAGCGACCGCTGTTGGGCTGCTTG 542
QY 1225 ATGCACTTGGGTAGAGCGCTATGTTGAAGTACCAACAGATTCATCAAACTGCTGCGC 1284
DB 543 ATGCACTTGGGTAGAGCGCTATGTTGAAGTACCAACAGATTCATCAAACTGCTGCGC 602
QY 1285 TTCCCTCAAGTACGAACATGGAATAATATCAAGGATCTTTGTTGGGAATCCCAATTG 1344
DB 603 TTCCCTCAAGTACGAACATGGAATAATATCAAGGATCTTTGTTGGGAATCCCAATTG 662
QY 1345 TCACCTATTGCTGCTGGGATCCGCTGATTTTGAATATCCGACTATCAAACTGATGAT 1404
DB 663 TCACCTATTGCTGCTGGGATCCGCTGATTTTGAATATCCGACTATCAAACTGATGATG 722
QY 1405 GCGAAGGGGTGGAACCTGGAACGATGCGATTCGCC 1439
DB 723 GCGAAGGGGTGGAACCTGGAACGATGCGATTCGCC 757

RESULT 13
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LOCUS CA327176
DEFINITION UT-M-FV0-ccy-c-24-0-UI.r1 NIH_BMAP_FY0 Mus musculus cDNA clone
IMAGE: 6826033 5', mRNA sequence.
CA327176
VERSION CA327176.1 GI:24545274
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgi.nci.nih.gov/
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Llin, University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

FEATURES
source
Seq primer: pyx-5
Location/Qualifiers
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/mol_type="mRNA"
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/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 13.5,14.5,16.5,17.5dpc"
/lab_host="DH10B (T1 phage resistant)"
/clone_1lb="NIH_BMAP_FY0"
/note="Organ: Brain; Vector: pyx-Asc; Site_1: Ecor I;
Site_2: Not I; The library was constructed according
to Honaido, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with Ecor I adaptor, digested with NotI and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is ACCGAGACAG. This library was created for the University
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the

Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."

Query Match 34.5%; Score 588.8; DB 14; Length 739;
Best Local Similarity 87.4%; Pred. No. 2.6e-161;
Matches 644; Conservative 0; Mismatches 93; Indels 0; Gaps 0;

ORIGIN
BASE COUNT 183 a 168 c 201 g 186 t 1 others
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DB 3 CTTGTCCTCCCTTCATATGGGGGACGAGATTCGTTGATGATGACTTCTGGGGAGACG 62
QY 635 AAAGCATCTGATGGCTCCCAAAAGCTTACCGGACTTGGCGTTAGAGAGGGGATCAAA 694
DB 63 AAAGCATCTGATGGCTCCCAAAAGCTTACCGGACTTGGCGTTAGAGAGGGGATCAAA 122
QY 695 CTCAGAAATTTGGCTCCCAAAAGTGGCCATGCTGCTATTTAACAAGCAGCCAGTTACT 754
DB 123 CTCAGAAATTTGGCTCCCAAAAGTGGCCATGCTGCTATTTAACAAGCAGCCAGTTACT 182
QY 755 TTGGGATGAAGATTTGGGGGTCCTTGCAGCAAGATGATGAGAGGATGAGAGGCA 814
DB 183 TTGGGATGAAGATTTGCAGATTTGCAGTCAAAAAGATGAGAGGATGAGAGGCA 242
QY 815 TGGAAGAGCTATTTCTCCAGAACACTGCTGCTGTTCTACCCAGATTTCCTC 874
DB 243 TGGAAGAGCTATTTCTCCAGAACACTGCTGCTGTTCTACCCAGATTTCCTC 302
QY 875 ATGCTGTAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 934
DB 303 ATGCTGTAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 362
QY 935 TTGATGTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 994
DB 363 TCATATGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 422
QY 995 CACTGAGACCACTTATTTCCGGGTAAAGGTGTAACAGATTTCCAGCTGACACC 1054
DB 423 CACTGAGACCACTTATTTCCGGGTAAAGGTGTAACAGATTTCCAGCTGACACC 482
QY 1055 ATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1114
DB 483 ATTAAGTATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 542
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DB 543 GGAACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 602
QY 1175 TCGCAGGCTCAGCGGCTGGTGGCATTTAGCGACGCTGTTGGGCTGCTGATGACACTTCG 1234
DB 603 TAGCTGGCTCAGCGGCTGGTGGCATTTAGCGACGCTGTTGGGCTGCTGATGACACTTCG 662
QY 1235 GTGAGAACGCTATGTTGAAGTACCAACAGATATCAAACTGCTGCTTCCCAAGT 1294
DB 663 GTGAGAACGCTATGTTGAAGTACCAACAGATATCAAACTGCTGCTTCCCAAGT 722
QY 1295 CAGAAGTGAAGATATC 1311
DB 723 CAGAAGTGAAGATATC 739
RESULT 14
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LOCUS CB202317
DEFINITION AGENCOURT_11288893 NIH_MGC_135 Mus musculus cDNA clone
IMAGE:30141583 5', mRNA sequence.
CB202317
VERSION CB202317.1 GI:28237404
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

1414920-1417991 and 1520904-1522439). Subtraction by Bento
Soares and M. Fatima Bonaldo. "
BASE COUNT 183 a 173 c 116 g 198 t
ORIGIN

Query Match 32.7%; Score 558; DB 9; Length 670;
Best Local Similarity 99.8%; Pred. No. 2.8e-132;
Matches 569; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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OY 47 TAGAGATTTTGGAGTATATCTCCACAAAAGCCAGAATATATTAATGGACATTCACCA 106
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Db 669 TAGAGATTTTGGAGTATATCT-CACAAAAGCCAGAATATATTAATGGACATTCACCA 611
OY 107 AGTATGAGCCCTGGCAGCTAATTCAGAGAGTGTCTGTGACCCCTGCTGATATGCTGGG 166
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Db 610 AGTATGAGCCCTGGCAGCTAATTCAGAGAGTGTCTGTGACCCCTGCTGATATGCTGGG 551
OY 167 GATATGAGTGTGCTTCCAGCCAGAGTATATGTCACAGCTTTAAAAAGAAATGTTTA 226
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Db 550 GATATGAGTGTGCTTCCAGCCAGAGTATATGTCACAGCTTTAAAAAGAAATGTTTA 491
OY 227 AGCTCACCAGAGAGATGCCATTTATTTGCTGTAAGTCAAGACAAAGTTGAACAAGACCA 286
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Db 490 AGCTCACCAGAGAGATGCCATTTATTTGCTGTAAGTCAAGACAAAGTTGAACAAGACCA 431
OY 287 AGGATGATATTTAGCAAGAACATGTCATTCCTGAAAGTGACAAAGATATGTGAAAGCTT 346
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Db 430 AGGATGATATTTAGCAAGAACATGTCATTCCTGAAAGTGACAAAGATATGTGAAAGCTT 371
OY 347 TACCTCCCAAGGCTGTGAGCTATCTGCTTTTGGAGAACTTAAGAGTACAGCTCTTA 406
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Db 370 TACCTCCCAAGGCTGTGAGCTATCTGCTTTTGGAGAACTTAAGAGTACAGCTCTTA 311
OY 407 TGGAGCCCTTTCGCAAGAGGAGAGCCCTGGAACAAGTACAGTGGGGAGAGAAAGC 466
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Db 310 TGGAGCCCTTTCGCAAGAGGAGAGCCCTGGAACAAGTACAGTGGGGAGAGAAAGC 251
OY 467 TCACGTGAGCTCCTTGTGAAGGCTTATGAGATTTTTCATGAGATAACCCCTGCATCCAG 526
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Db 250 TCACGTGAGCTCCTTGTGAAGGCTTATGAGATTTTTCATGAGATAACCCCTGCATCCAG 191
OY 527 ATATCTCCAGAGACTAGCAAGATAGAGGCAAAATGCTAGGATAGCTTTTCCCTGT 586
    |||||||
Db 190 ATATCTCCAGAGACTAGCAAGATAGAGGCAAAATGCTAGGATAGCTTTTCCCTGT 131
OY 587 TCAATGGGGGACCAGATTGCTGTGGATGTG 616
    |||||||
Db 130 TCAATGGGGGACCAGATTGCTGTGGATGTG 101
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Search completed: October 6, 2003, 13:31:11
Job time : 3757 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 6, 2003, 08:56:50 ; Search time 6316 Seconds

(Without alignments)
11056.481 Million cell updates/sec

Title: US-10-053-510-7

Perfect score: 1707
Sequence: 1 atgcctagacagacctctc.....gttcctcaaaacccactga 1707

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapept 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_cm:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
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23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
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28: em_un:*
29: em_vl:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
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41: em_higo_other:*
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1707	100.0	1707	6 AR220089	AR220089 Sequence
2	1707	100.0	1707	6 AR267065	AR267065 Sequence
3	1707	100.0	1707	6 BD081354	BD081354 Sequence
4	1702.2	99.7	1707	6 AF144638	AF144638 Homo sapi
5	1699	99.5	2130	6 AR282336	AR282336 Sequence
6	1699	99.5	2130	6 AX019488	AX019488 Sequence
7	1699	99.5	2130	6 BD107922	BD107922 Novel com
8	1699	99.5	4701	9 BC052991	BC052991 Homo sapi
9	1699	99.5	5741	9 AB033078	AB033078 Homo sapi
10	1694.2	99.3	2131	9 HSA011304	AJ011304 Homo sapi
11	1297.4	76.0	2033	10 RN0512838	AJ512838 Rattus no
12	1283	75.2	4108	10 BC026135	BC026135 Mus muscu
13	1278.2	74.9	1707	6 AR220088	AR220088 Sequence
14	1278.2	74.9	1707	6 AR267064	AR267064 Sequence
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16	1278.2	74.9	1911	10 AF036894	AF036894 Mus muscu
17	1217	71.3	1467	6 AR220092	AR220092 Sequence
18	1217	71.3	1467	6 AR267066	AR267066 Sequence
19	1217	71.3	1467	6 BD081357	BD081357 Sphingosl
20	438	26.8	2297	3 AK112751	AK112751 Ciona int
21	401.6	23.5	2043	3 AY052075	AY052075 Drosophila
22	401.6	23.5	2060	6 AX151205	AX151205 Sequence
23	398.4	23.3	1966	3 DME297394	AJ297394 Caenorhab
24	295.8	17.3	1659	3 AF144639	AF144639 Sequence
25	284.4	16.7	785	6 AR282337	AR282337 Sequence
26	284.4	16.7	785	6 AX019490	AX019490 Sequence
27	284.4	16.7	785	6 BD107923	BD107923 Novel com
28	256.2	15.0	1770	6 AR220091	AR220091 Sequence
29	256.2	15.0	1770	6 AR267067	AR267067 Sequence
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31	256.2	15.0	2270	6 AX072946	AX072946 Sequence
32	256.2	15.0	24942	8 YSCD9819	Y51031 Saccharomyc
33	250	14.6	1666	8 AY113914	AY113914 Arabidops
34	250	14.6	1836	8 AF360166	AF360166 Arabidops
35	241	14.1	169772	9 AC069538	AC069538 Homo sapi
36	241	14.1	175731	9 AC073176	AC073176 Homo sapi
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38	241	14.1	259210	2 AC073368	AC073368 Homo sapi
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40	225.6	13.2	1629	6 AR220090	AR220090 Sequence
41	225.6	13.2	1629	6 AR267066	AR267066 Sequence
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43	224.4	13.1	73721	2 AC020007	AC020007 Drosophila
44	224.4	13.1	163072	3 AC099032	AC099032 Drosophila
45	224.4	13.1	170994	3 AC007520	AC007520 Drosophila

ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
AR220089	AR220089	Sequence 3 from patent US 6423527.	AR220089	AR220089.1	GI:23324515	Unknown.	Unknown.	1 (bases 1 to 1707)	Saba,J.D. and Zhou,J.	Sphingosine-1-phosphate lyase polypeptides, polynucleotides and modulating agents and methods of use therefor	Patent: US 6423527-A 3 23-JUL-2002;
AR220089	AR220089	Sequence 3 from patent US 6423527.	AR220089	AR220089.1	GI:23324515	Unknown.	Unknown.	1 (bases 1 to 1707)	Saba,J.D. and Zhou,J.	Sphingosine-1-phosphate lyase polypeptides, polynucleotides and modulating agents and methods of use therefor	Patent: US 6423527-A 3 23-JUL-2002;

Pred. No. is the number of results predicted by chance to have a

FEATURES		Location/Qualifiers			
SOURCE	1. 1707 /organism="unknown"				
BASE COUNT	467 a 388 c 424 g 428 t				
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Best Local Similarity 100.0%; Pred. No. 0;					
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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DB	1	ATGCCCTAGACAGACCTTCTGATGTGTAAGGCTTTGAGCCCTACTTATGAGATTTTGGAA	60		
QY	61	GTATATCTCACAAAGCCAGAAATTATGTAAATGACATTGACCAAGTATGAGCCCTGG	120		
DB	61	GTATATCTCACAAAGCCAGAAATTATGTAAATGACATTGACCAAGTATGAGCCCTGG	120		
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QY	241	ATGCCCATTTATGTCCTGTAAGATTCAGACAAAGTTGAACAAGCCAAAGATGATTTAGC	300		
DB	241	ATGCCCATTTATGTCCTGTAAGATTCAGACAAAGTTGAACAAGCCAAAGATGATTTAGC	300		
QY	301	AAGAACATGTCATTCTCGAAAGTGAGACAAAGATGTAAGTAAAGCTTTACCTCCAGAGGT	360		
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DB	481	GTCGAAGCTTATGAGAAATTTTGCATGTGAGATTAACCCCTGCATCCAGATATCTTCCAGGA	540		
QY	541	CTACGCAAGATAGAGCGAGAAATGTAGAGTATACCTTGTCCCTGTTCAATGAGGGAGCA	600		
DB	541	CTACGCAAGATAGAGCGAGAAATGTAGAGTATACCTTGTCCCTGTTCAATGAGGGAGCA	600		
QY	601	GATTCGTGTGAGTGTGACTCTTGGGGGGAACAGAAAGCATATCTATGAGCCCTGCAAGCA	660		
DB	601	GATTCGTGTGAGTGTGACTCTTGGGGGGAACAGAAAGCATATCTATGAGCCCTGCAAGCA	660		
QY	661	TGTCGGATCTGGCCTTTGAGAAAGGGGATCAAACTCCAGAAATTTGCGCTCCCAAGT	720		
DB	661	TGTCGGATCTGGCCTTTGAGAAAGGGGATCAAACTCCAGAAATTTGCGCTCCCAAGT	720		
QY	721	GCCCATCTGCATTTAACAAAGCAGCCAGTACTTTGGAGTGAAGATTGTGCGGGTCCCA	780		
DB	721	GCCCATCTGCATTTAACAAAGCAGCCAGTACTTTGGAGTGAAGATTGTGCGGGTCCCA	780		
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DB	841	GCCATGCTCTGTCTTACCCCAAGTTTCTCATGGTGAATAGATCTGTCCCTGAA	900		
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Db		1081	TCAATCATTTGGTGTGTATAGTGACAAGAAGTACAGAACTATCAAGTTCTTGGTGAATACA	1140
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Db		1141	GATTGGCAGSGGTGCATCTATGCTTCCCACACATGCGAGGCTACGSGCCGTGGGCATT	1200
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DEFINITION	Sequence 3 from patent US 6495359.			linear
ACCESSION	AR267065			PAT 10-Apr-2003
VERSION	AR267065.1			
KEYWORDS	.			
SOURCE	Unknown.			
ORGANISM	Unknown.			
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AUTHORS	1 (bases 1 to 1707)			
TITLE	Saba,J.D. and Zhou,J.			
JOURNAL	Shlingosine-1-phosphate lyase polypeptides and			
FEATURES	modulating agents and methods of use therefor			
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Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
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DEFINITION Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor.
ACCESSION BD081354
VERSION BD081354.1 GI:22626957
KEYWORDS JP 2001518303-A/2.
SOURCE unclassified
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1707)
AUTHORS Saba,J.D. and Zhou,J.
TITLE Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor
JOURNAL Patent: JP 2001518303-A 2 16-OCT-2001;
CHILDREN'S HOSPITAL MEDICAL CENTER OF NORTHERN CALIFORNIA
OS Unidentified
PN JP 2001518303-A/2
PD 16-OCT-2001
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PI JULIE D SABA, JIANHUI ZHOU
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ACCESSION AF144638
VERSION AF144638.1 GI:5532486
KEYWORDS
SOURCE Homo sapiens (human)
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AUTHORS 1 (bases 1 to 1707)
Zhou J. and Saba J.
TITLE Cloning and characterization of human sphingosine-1-phosphate lyase gene
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1707)
AUTHORS Zhou J. and Saba J.
TITLE Direct Submission
JOURNAL Submitted (20-APR-1999) Research, Children's Hospital Oakland Research Institute Oakland Research Institute Oakland, 747 Fifty Second Street, Oakland, CA 94609-1809, USA
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LOCUS AR282336
DEFINITION Sequence 1 from patent US 6521437.
ACCESSION AR282336
VERSION AR282336.1 GI:29718395
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2130)
AUTHORS Duckworth,D.M., Godden,R.J. and Testa,T.T.
TITLE Human sphingosine lyase polypeptides
JOURNAL Patent: US 6521437-A 1 18-FEB-2003;
FEATURES Location/Qualifiers
source 1..2130

BASE COUNT 563 a 479 c 561 g 527 t
ORIGIN

Query Match 99.5%; Score 1699; DB 6; Length 2130;
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RESULT 6
AX019488

LOCUS AX019488 2130 bp DNA linear PAT 07-SEP-2000
DEFINITION Sequence 1 from Patent WO938983.
ACCESSION AX019488
VERSION AX019488.1 GI:10043420
KEYWORDS
SOURCE homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

REFERENCE
AUTHORS 1 Duckworth,D.M., Godden,R.J. and Testa,T.T.
TITLE Novel sphingosine-1 phosphate lyase
JOURNAL Patent: WO 938983-A 1 05-AUG-1999;
SMITHKLINE BECHAM PLC (GB)
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BD107922
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DEFINITION Novel compounds.
ACCESSION BD107922
VERSION BD107922.1 GI:23202740
KEYWORDS JP 2002501751-A/1.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 2130)
Duckworth,D.M., Godden,R.J. and Testa,T.T.
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PN JP 2002501751-A/1
PD 22-JAN-2002
PE 24-DEC-1998 JP 2000529442
PR 29-JAN-1998 EP 98300625.5,03-NOV-1998 GB 9824026.0 PI
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ORIGIN
Query Match 99.5%; Score 1699; DB 6; Length 2130;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
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Db		1858	ATGAATGGTTCGCCAAAAACCCCACTGA 1884	
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LOCUS				
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VERSION	BC052991.1	GI:31418632		
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SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
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	Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,			
	Klausner,R.D., Collins,F.S., Wagner,L., Shenmer,C.M., Schuler,G.D.,			
	Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.J., Bat,N.K.,			
	Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J.J., Hsieh,F.,			
	Datchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,			
	Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,			
	Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Tosilinski,S.,			
	Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,			
	Abraham,R.D., Mullahy,S.J., Bosak,S.A., McKean,P.J.,			
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	Wotley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Huliy,S.W.,			
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	Faney,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S.,			
	Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,			
	Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,			
	Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,			
	Butterfield,V.S., Krzywinski,M.I., Skalska,U., Smalls,D.E.,			
	Scherich,A., Schein,J.E., Jones,S.J., and Marra,M.A.			
TITLE	Generation and initial analysis of more than 15,000 full-length			
JOURNAL	human and mouse cDNA sequences			
PUBMED	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)			
	12477932			

REFERENCE	2 (bases 1 to 4701)
AUTHORS	Strausberg, R.
TITLE	Direct Submission
JOURNAL	Submitted (02-JUN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.ncl.nih.gov
COMMENT	Contact: MGC help desk Email: cgabds-remail.nih.gov Tissue Procurement: ATCC/DCDP/DHP cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www.simgc.stanford.edu Contact: (Dickson, Mark) mcdbaxil@stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	<p>Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAC Plate: 110 Row: k Column: 18 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 10190652.</p> <p>Location/Qualifiers</p> <p>1..4701</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="MGC:60255 IMAGE:6150776"</p> <p>/tissue_type="Skin, melanotic melanoma."</p> <p>/clone_id="NIH_MGC_72"</p> <p>/lab_host="DH10B"</p> <p>/note="Vector: pCMV-SPORT6"</p> <p>1..4701</p> <p>/gene="SGP1"</p> <p>/note="synonyms: SPL, KIAA1252"</p> <p>/db_xref="LocusID:8879"</p> <p>/db_xref="MIM:603729"</p> <p>211..1917</p> <p>/codon_start=1</p> <p>/product="SGP1 protein"</p> <p>/protein_id="AAH52991.1"</p> <p>/db_xref="GI:31418633"</p> <p>/db_xref="LocusID:8879"</p> <p>/translation="MPSDILMLKAFEPYLEILEVSTKAKNVYGHCTKYEPMOLIAWSYVWILLVWGVEFVROPESLWREKPKCKLTKRPDITGRKLODKLNTKDISKNMSFLVVKREYKALPSQGLSSAVLELKEYSSMDATWGRASGYISGEEKITELLVKAVGDFAWMSPLHPDIFEPGLRTIEAVINRAASGLFNGDSCCVSGTESTILMACKAYADLAEFKGIKPTPEIAPQSAHAENKASYGMKIVRPPLTKMNEVVRAMRAIRSRNPAALVCSSTPQPHGVDPPEVAKLAVKYPKPLHVDACLGFLIVEMKAGYPLEHPPEFRKGVSTISADPHKGVAKGVAKSSLVLYSDKRNVOFVDTDMOGGIVASPTIAGSGRGGISAAACAAALMHFGENGCVENATKOITKARLKELEMIKIPVFNQPLSVTQDSKPFDIRLSNMLTAKGWNLNLOLFPSTHFCITLLHARRAIVQLKDIRESYIOLSKNPRAKTTGMAIYGAQWTVDMVAELSSVFLDSLSTDTVTVQSNMGSPKPH"</p>
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Db 1291 TCATCATTTGCTTTATAGTACAAAGATACAGGAATACATTCCTTCGTGATACA 1350
OY 1141 GATTGGCAGGGTGCATCTATCTTCCCAACATCGAGGCTCAGGGCTGTGGCAT 1200
Db 1351 GATTGGCAGGGTGCATCTATCTTCCCAACATCGAGGCTCAGGGCTGTGGCAT 1410
OY 1201 AGCGAGGCTGTTGGGCTGCTTATGACACTTCGGTGAGAAAGGCTATGTAAGCTACC 1260
|||||

Db 1411 AGCGAGGCTGTTGGGCTGCTTATGACACTTCGGTGAGAAAGGCTATGTTAGCTACC 1470
OY 1261 AAACAGATCATCAAACTGCTGCTCTCAAGTCAAGAACTGAAATATCAAAAGCATC 1320
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OY 1321 TTTGTTTTTGGGAATCCCAATTGTCACATTTGCTCTGGGATCCCGTATTTTGCATC 1380
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Db 1771 GGAATGGGTCATCTATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATGCTGATG 1830
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Db 1831 TTTGCTCTGATCTTCTTGAGACAGCTTGTACAGACACCGACAGCTGTACACCCAGGACGCCAG 1890
OY 1681 ATGAATGGTTCTTCCAAACCCGACCTGA 1707
Db 1891 ATGAATGGTTCTTCCAAACCCGACCTGA 1917

RESULT 9
AB033078
LOCUS
DEFINITION
AB033078
AB033078
VERSION
AB033078.1
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
Nagase,T., Ishikawa,K., Kikuno,R., Hirose,M., Nomura,N. and
Ohara,O.
1 (sites)
TITLE
Prediction of the coding sequences of unidentified human genes. XV.
The complete sequences of 100 new cDNA clones from brain which code
for large proteins in vitro
JOURNAL
DNA Res. 6 (5), 337-345 (1999)
MEDLINE
20039619
PUBMED
10574462
REFERENCE
2 (bases 1 to 5741)
AUTHORS
Ohara,O., Nagase,T. and Kikuno,R.
TITLE
Direct Submission
JOURNAL
Submitted (04-OCT-1999) Osamu Ohara, Kazusa DNA Research Institute,
Laboratory of DNA Technology; 1532-3 Yana, Kisarazu, Chiba
292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp,
URL:ftp://www.kazusa.or.jp/huge/, Tel:+81-438-52-3913,
Fax:+81-438-52-3914)
FEATURES
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/clone="h09572"
/tissue_type="brain"
/clone_lib="pbluescriptII SK plus"
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CDS
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/note="Start codon is not identified."
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/product="K1A1252 protein"
/protein_id="BAA8566.1"
/db_xref="GI:6330874"
/translation="KRGARGGKMRKMPSTDLMLKAFPEYLEILEYVSTKKNVNG
HCTKEPMOLIAWSVWTLIIWVGEFVPPESIMSRKKCEKRLPKMBILIRKID
KLNKTRDDISKNSFLKVDKEYKALPDSGLSSAVLEKLEKESMDAPQEBRSGT
VISEERLELLKAIKIDFAMSNPLHPDIPGLKLEAETVRLACSLFENGPOSCGV
TSGESTISLMACKAYRDLAEKIKTPEIYAPQSAHAFAKASVEMKIVRPLETM
MEVDVAMRAIRANTAMLCSTPOEPHFVIDPEYAKLAVKXKILADACIGEL
IYMEKAGVPLEHPEDPRKVSISADTHGYAPGSLVYSOKKYNOPEVDT
DMOGIYASPTIISPRGGSISACMAALHMGNGVYEATKOIITKRLKSELENK
GIRFVGNPOLSVIALSRRPDITRLSLMTAKMNLQLOPPSIHCITLILARKRY
AIOFLKIDRESVQIMKNPKAKTTGMAIYGMATTVDRMVAVELLSVFLDSLYSTD
VTGDSOMNSPKPH"

BASE COUNT 1369 a 1323 c 1386 g 1663 t

ORIGIN

Query Match 99.5% Score 1699; DB 9; Length 5741;
Best Local Similarity 99.7% Pred. No. 0;
Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

1 ATGCGTACACAGACCTTCTGATGTTGAAGCCCTTGAAGCCCTTCTGATGATTTGGAA 60
201 ATGCGTACACAGACCTTCTGATGTTGAAGCCCTTCTGATGATTTGGAA 260
61 GTATCTCCACAAAAGCAGAAATTAATGTAATGACATTCACCAAGTATGAGCCCTGG 120
261 GTATCTCCACAAAAGCAGAAATTAATGTAATGACATTCACCAAGTATGAGCCCTGG 320
121 CACCTAATTCAGATGATGTCGTGTGACCCCTGCTGATGATCTGCGGATATGAGTTGTC 180
321 CACCTAATTCAGATGATGTCGTGTGACCCCTGCTGATGATCTGCGGATATGAGTTGTC 380
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381 TTCCAGCCAGAGATTTATGTCAGGTTTAAAAAGAAATGTTTAAAGTCACACGAGAAG 440
241 ATGCCCATTTATGTCGTGTAAGATTCAAGACAGTTGAACAAGCAAGATGATATTAGC 300
441 ATGCCCATTTATGTCGTGTAAGATTCAAGACAGTTGAACAAGCAAGATGATATTAGC 500
301 AAGAACATGTCATTCCTGAAAGTGAGCAAAAGATATGTAAGCTTAACTCCAGAGGT 360
501 AAGAACATGTCATTCCTGAAAGTGAGCAAAAGATATGTAAGCTTAACTCCAGAGGT 560
361 CTGAGCTCATCTGCTGTTTGGAGAAACTTAAGAGATACAGCTTATGAGAGCCCTTGG 420
561 CTGAGCTCATCTGCTGTTTGGAGAAACTTAAGAGATACAGCTTATGAGAGCCCTTGG 620
421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAGACTCACTGAGCTCCTT 480
621 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAGACTCACTGAGCTCCTT 680
481 GTGAAGGCTTATGAGAGTTTTCGATGAGTAAACCCCTGATCGACATATCTTCCAGGA 540
681 GTGAAGGCTTATGAGAGTTTTCGATGAGTAAACCCCTGATCGACATATCTTCCAGGA 740
541 CTACGCAAGATAGAGCAGAAATTTGAGATAGCTTTCCCTGTTCAATGGGGAGCA 600
741 CTACGCAAGATAGAGCAGAAATTTGAGATAGCTTTCCCTGTTCAATGGGGAGCA 800
601 GATTCTGTGATGTGTGACTTCTGGGGAAACAGAAAGCATACTCATGAGCTCGCAAGCA 660
801 GATTCTGTGATGTGTGACTTCTGGGGAAACAGAAAGCATACTCATGAGCTCGCAAGCA 860
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861 TTGCGGATCTGGCCTTTGAGAAAGGAGTCAAAAATCTCAGAAATTTGGCTCCCAAGT 920

721 GCCCATCTGCATTTTAAACAAAGCAGCCAGTTACTTTGGAGTGAAGATTGTGCGGCTCCA 780
921 GCCCATCTGCATTTTAAACAAAGCAGCCAGTTACTTTGGAGTGAAGATTGTGCGGCTCCA 980
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841 GCCATGCTGCTGCTTCTTACCCCACTTTCCATATGTTGAATAGATCCGTCCCGAA 900
1041 GCCATGCTGCTGCTTCTTACCCCACTTTCCATATGTTGAATAGATCCGTCCCGAA 1100
901 GTGGCCAAAGTGGCTGTCAATATCAAAATACCCCTTATGTCGACGCTTGTCTGGAGGC 960
1101 GTGGCCAAAGTGGCTGTCAATATCAAAATACCCCTTATGTCGACGCTTGTCTGGAGGC 1160
961 TTCCCTATGCTCTTTATGAGAAAGCAGATACCCACTGTGAGCAGCAGCTATTTCCGG 1020
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1021 GTGAAAGTGTAAACACATTTTCAGCTGACACCCATAGTATGCTATGCCCAAAAGGC 1080
1221 GTGAAAGTGTAAACACATTTTCAGCTGACACCCATAGTATGCTATGCCCAAAAGGC 1280
1081 TCATCATTTGGTGTATGATGACAAAGATGACAGAACTATCAGTTCTTCTGATGATCA 1140
1281 TCATCATTTGGTGTATGATGACAAAGATGACAGAACTATCAGTTCTTCTGATGATCA 1340
1141 GATTGGAGGGTGCATCTATGCTTCCCAACATGCGAGGCTCAGGCGCTGTGGCATTT 1200
1341 GATTGGAGGGTGCATCTATGCTTCCCAACATGCGAGGCTCAGGCGCTGTGGCATTT 1400
1201 AGCGCAGCTGTGGGCTGCTGATGACACTTGGGTGAGAAAGGCTATGTTGAAGCTAAC 1260
1401 AGCGCAGCTGTGGGCTGCTGATGACACTTGGGTGAGAAAGGCTATGTTGAAGCTAAC 1460
1261 AAACAGATCATCAAAACTGCTCGCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1320
1461 AAACAGATCATCAAAACTGCTCGCTCTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 1520
1321 TTGTTTTGGGAAATCCCAATTTGTCATCTATGCTCTGCGATCCCGTATTTTGACATC 1380
1521 TTGTTTTGGGAAATCCCAATTTGTCATCTATGCTCTGCGATCCCGTATTTTGACATC 1580
1381 TACGAGATTCACAACTGATGACCTGCTAAGGGGTGGAACCTTGAAACCACTTGCAATTC 1440
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1441 CCCAGTATTCATTTCTGATCACAATTAACAGCCCGGAAAGCAGTATGATCAATTC 1500
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1501 CTAAAGGACATTCGAGATCTGTCACATCAATTCATGAAGATCTTAAAGCGAAGACACA 1560
1701 CTAAAGGACATTCGAGATCTGTCACATCAATTCATGAAGATCTTAAAGCGAAGACACA 1760
1561 GGAATGGGTGCAATCTATGATGAGTGGCCAGCAACTGTGACAGAAATATGTTGTCAGAA 1620
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1621 TTGTCCTCAGTCTTCTTGAAGCTTGTACAGCAGCAGCACTGTACCCAGGGAGCAG 1680
1821 TTGTCCTCAGTCTTCTTGAAGCTTGTACAGCAGCAGCACTGTACCCAGGGAGCAG 1880
1681 ATGAATGTTCTCCAAAACCCCACTGA 1707
1881 ATGAATGTTCTCCAAAACCCCACTGA 1907

RESULT 10
HSA011304 2131 bp mRNA linear PRI 14-SEP-2000
LOCUS
DEFINITION Homo sapiens mRNA for sphingosine-1-phosphate lyase.

ACCESSION	AJ011304
VERSION	AJ011304.2
KEYWORDS	sphinganine-1-phosphate aldolase; sphingosine-1-phosphate lyase.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi; Mammalia: Eutheria: Primates: Catarrhini: Homnidae: Homo.
AUTHORS	Van Veldhoven, P. P., Gijbers, S., Mannaerts, G. P., Vermeesch, J. R. and Brys, V.
TITLE	Human sphingosine-1-phosphate lyase: cDNA cloning, functional expression studies and mapping to chromosome 10q22(1)
JOURNAL	Biochim. Biophys. Acta 1487 (2-3), 128-134 (2000)
MEDLINE	204771968
PUBMED	11018465
REFERENCE	2
AUTHORS	Van Veldhoven, P. P.
TITLE	Direct Submission
JOURNAL	Submitted (16-SEP-1998) Van Veldhoven P. P., Campus Gasthuisberg - Moleculaire Celbiologie - Farmakologie, Katholieke Universiteit Leuven, Herestraat, B-3000, BELGIUM
REMARK	Revised by [3]
REFERENCE	3 (bases 1 to 2131)
AUTHORS	Van Veldhoven, P. P.
TITLE	Direct Submission
JOURNAL	Submitted (11-SEP-2000) Van Veldhoven P. P., Campus Gasthuisberg - Moleculaire Celbiologie - Farmakologie, Katholieke Universiteit Leuven, Herestraat, B-3000, BELGIUM
COMMENT	On Sep 14, 2000 this sequence version replaced gi:4160531.
FEATURES	Location/Qualifiers
Source	1..2131
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ORIGIN	
Query Match	99.3%; Score 1694.2; DB 9; Length 2131;
Best Local Similarity	99.5%; Pred. No. 0;
Matches 1699; Conservative	0; Mismatches 8; Indels 0; Gaps 0;
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Db	ATGCTTACACAGACTTCGATGTGTAAGGCCCTTGAGCCCTCCTTAGAGATTGGA 237
Oy	178 ATGGCTGACACAGAAAGCCAGAATAATGTAAATGACATTCACCACAAGTATGAGCCCTGG 120
Db	ATGGCTGACACAGAAAGCCAGAATAATGTAAATGACATTCACCACAAGTATGAGCCCTGG 297
Oy	61 GTATACCTCACAAAAGCCAGAATAATGTAAATGACATTCACCACAAGTATGAGCCCTGG 120
Db	GTATACCTCACAAAAGCCAGAATAATGTAAATGACATTCACCACAAGTATGAGCCCTGG 297
Oy	121 CAGCTAATTCAGTGGAGTGTGTGTGACACCCTGCTGATAGTCTGGGATATGAGTTGTC 180
Db	CAGCTAATTCAGTGGAGTGTGTGTGACACCCTGCTGATAGTCTGGGATATGAGTTGTC 180

Db	298	CAGCTAATGCATGAGAGCTGCTGTGGACCCCTGCGTAATGCTGGGATATGAGATTGTGTC	357
Oy	181	TTCCAGCCGACGAGCTTATGCTCAAGGTTTAAAAAGAAATCTTTTAAGCTCACGAGAG	240
Db	358	TTCCAGCCGACGAGATTATGCTCAAGGTTTAAAAAGAAATGTTTTTAAGCTCACGAGAG	417
Oy	241	ATGCCCATATTGGTCGTAAAGTTCACGACAGAAGTTGAAACAAGACAGATGATATTAGC	300
Db	418	ATGCCCATATTGGTCGTAAAGTTCACGACAGAAGTTGAAACAAGACAGATGATATTAGC	477
Oy	301	AAGAAACATGTCATTCTCGTAAAGCTGGACAAAGATATGTGAAAGCTTTACCTCCAGGGT	360
Db	478	AAGAAACATGTCATTCTCGTAAAGCTGGACAAAGATATGTGAAAGCTTTACCTCCAGGGT	537
Oy	361	CTGAGCTCATTCGCTGTTTGTGAGAACTTAAGAGATACAGCTCTATGAGCGCTTCTGG	420
Db	538	CTGAGCTCATTCGCTGTTTGTGAGAACTTAAGAGATACAGCTCTATGAGCGCTTCTGG	597
Oy	421	CAAGAGGGGAAGCGCTCGGAACAGTGTACAGTGGGAGGAGAAAGCTCACAGACTCCTT	480
Db	598	CAAGAGGGGAAGCGCTCGGAACAGTGTACAGTGGGAGGAGAAAGCTCACAGACTCCTT	657
Oy	481	GTGAAGGCTTATGAGATATTTGCAATGAGTAACCCCTGCATCCAGATATTCTCCAGGA	540
Db	658	GTGAAGGCTTATGAGATATTTGCAATGAGTAACCCCTGCATCCAGATATTCTCCAGGA	717
Oy	541	CTAGCGCAAGATAGAGGCGAGAAATTGTGAGATAGCTTGTCCCTTCATGAGGGGAGCA	600
Db	718	CTAGCGCAAGATAGAGGCGAGAAATTGTGAGATAGCTTGTCCCTTCATGAGGGGAGCA	777
Oy	601	GATTGCTGTGATGTGTGACTTCTTGGGGGGAACAGAAAGCTATCTCATGTGCTCGAAAGCA	660
Db	778	GATTGCTGTGATGTGTGACTTCTTGGGGGGAACAGAAAGCTATCTCATGTGCTCGAAAGCA	837
Oy	661	TGTGGGGATCTGGGCTTTGAGAAAGGGGATCAAAACTCCAGAAATTGTGGCTCCCAAGT	720
Db	838	TATGGGATCTGGGCTTTGAGAAAGGGGATCAAAACTCCAGAAATTGTGGCTCCCAAGT	897
Oy	721	GCCCATGCTGATTTAACAAAGCAGCCAGTTACTTTGGGATGAAGATTGTGCGGGTCCCA	780
Db	898	GCCCATGCTGATTTAACAAAGCAGCCAGTTACTTTGGGATGAAGATTGTGCGGGTCCCA	957
Oy	781	TTGACGAGAAGATGATGAGAGTGGATGTGAGGGCAATGAGAGAAGCTATCTCAGAGAACCT	840
Db	958	TTGACGAGAAGATGATGAGAGTGGATGTGAGGGCAATGAGAGAAGCTATCTCAGAGAACCT	1017
Oy	841	GCCATGCTGCTGTGTTTACCCCAAGTTCCTCATGGTGTAAATGATCCGTGCCCTGAA	900
Db	1018	GCCATGCTGCTGTGTTTACCCCAAGTTCCTCATGGTGTAAATGATCCGTGCCCTGAA	1077
Oy	901	GTTGGCCAAGCTGCGTGTCAAAATACAAATACCCCTTCATGTGCGAGCGTTGTCTGGGAGGC	960
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Db	1318	GATTGGCAGGGTGGCATCTATGCTTCCCAACATCGCAGGCTCAGGGCTGTGGGCATT	1377
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Db	970	GCATGCGTGGCTGTTCGGCCCAACAGTTTCCATGATGATGATGATCCATATCCCGAA	1029
Qy	901	GTGGCCAAAGCTGGCTGTCAAAATACAAAATACCCCTTATGTGCAGCCTTGTCTGGAGGC	960
Db	1030	GTGGCCAAAGCTGGCTGTCAAAATATATAAATCCCATTCATGTGGATGTCTGTCTTGGGGGC	1089
Qy	961	TTCTCATTCGCTTTATGGAGAAAGCAGGATACCCACTGGGAGCACCATTGTGATTTCCGG	1020
Db	1090	TTCTCATTTGCTTTCATGTAGAGAAAGCAGGATACCCACTGGGAGAAACATTGTGATTTCCGG	1149
Qy	1021	GTGAAGGTGTAAACCAGCATTTACGCTGACACCCCATAAATATGAGCTATGCCCAAAAGC	1080
Db	1150	GTGAAGGTGTGACACCATTTACAGAGATACATATAGTACGGCTATGCTCCAAAGGT	1209
Qy	1081	TCATCATTTGGTGTGTATAGTGACAAAGATACAGAAATCATATCATTTCTTGCTGATACA	1140
Db	1210	TCATCATGTTGGATGTACTCTTAACGAGAGATACAGAAATCAAGTTCTTTGTTGATGCA	1269
Qy	1141	GATTGGCAGGGTGGCATCTATGCTTTCCCAACCATCGCAGGCTACGCGCTGGTGGCATT	1200
Db	1270	GATTGGCAGGGTGGCATCTACGATCTACGATCTCCAGCATATAGTGGCTACGCGCTGGTGGCATC	1329
Qy	1201	AGCCGACGCTTGTGGCTGCTTGATGCATCTTCCGTGAGAAAGGCTATGTTGAAGTACC	1260
Db	1330	ATTTCACAGCTGTTGGCGCCCTTGATGACACTTTGGTGAAGCGGCTATGTTGAAGTACC	1389
Qy	1261	AAACAGATCATCAAAACCTGTCGGTTCCTCAAGTCAGAACTGAGAAATATCAAAAGCATC	1320
Db	1390	AAACAGATCATCAAAACCTGCTCGTCTCTCAAGTCAGAACTGAGAAATATCAAAAGCATC	1449
Qy	1321	TTTTGTTTTGGGAATCCCAATTTGCACTATTCCTCTGGGATCCCGTATTTGACATC	1380
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Qy	1381	TACCGACTATCAAAACCTGATGACGTGCTTAAGGGGTGAACTTGAACCACTTGCATTTCCA	1440
Db	1510	TACCGACTATCTAATATGATGTCTGCTTAAGGGGTGAAATTTAATCTCTTGCATTTCCA	1559
Qy	1441	CCCGATTTTCATTTCTGATCACAATTAACACCCCGGAAACAGTATACAAATTC	1500
Db	1570	AGAGCATTTCAATTTCTGCATTAAGTTAGTACATCTGGAAGCAAGTGGCAATCCACTTC	1629
Qy	1501	CTAAGAGCATTCGAGAATCTGTCACTCAATCATATGAAGATCTCTAAGCAGACACA	1560
Db	1630	CTAAGAGATATCCGGAGATGGGTACACAAATCATGAAGATCTCTAAGCATGAACACA	1689
Qy	1561	GGATGGGTGCATCTATGCCATGGCCACAGCAACTGTGACAGAAATATGTTGGACAA	1620
Db	1690	GGATGGGTGCATCTATGGCATGGCCACAGCAACATTGACAGAAAGATGTGTGCAGAA	1749
Qy	1621	TTGTCTCAAGTCTTCTTGGACAGCTTGTACAGCAACGACATGTCAACCGAGGACGACG	1680
Db	1750	ATATCTCTCGGCTCTTGGACAGGCTTTATGTACAGCCCTGTGACTCAGGGTAACAG	1809
Qy	1681	ATGAATGGTCTCCAAACCCCACTGA	1707
Db	1810	ATGAACGGTCTCCAAAGCCCGGTGA	1836

RESULT 12	LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS
BC026135	BC026135	4108 bp mRNA linear ROD 16-APR-2003	BC026135	Mus musculus sphingosine phosphate lyase 1, mRNA (cdna clone	BC026135	GI:20072150	Mus musculus (house mouse)	Mammalia: Eutheria: Rodentia: Sclurognathii: Muridae: Murinae: Mus.	Strasberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,

TITLE
JOURNAL
MEDLINE PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D., Altschul S.F., Zeeberg B., Blueton K.H., Schaefter C.E., Bhac N.K., Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Biel E., Ditachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Donald O.F., Casavant T.L., Schneitz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Moley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.R., Muzny D.M., Sodergren E.T., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Young A.C., Shenchenko Y., Sanchez A., Whiting M., Madan A., Young A.C., Shenchenko Y., Boffard G.G., Bladesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimmwood J., Schmutz J., Myers R.M., Butcherfield Y.S., Krzywinski M.I., Skalska U., Smalls D.E., Schnerich A., Schein J.E., Jones S.J. and Marr M.A. Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences <i>Proc. Natl. Acad. Sci. U.S.A.</i> 99 (26), 16899-16903 (2002) 22388257 12477932 2 (bases 1 to 4108)
Straussberg,R Direct Submission Submitted (02-APR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2550, USA NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgaps-remail.nih.gov Tissue Procurement: Jeffrey E. Green, M.D. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E Consortium (LILN) DNA Sequencing by: Institute for Systems Biology http://www.systemsbio.org contact: amadansystemsbiology.org Anup Madan, Jessica Fahey, Erin Helton, Mark Ketteman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whitting
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E Consortium/LNL at: http://Image.lnl.gov Series: IRAC File# 18 Row: 0 Column: 1 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6677926. Location/Qualifiers 1. .4108 /organism="Mus musculus" /mol_type="mRNA" /strain="FVB/N" /db_xref="taxon:10090" /clone="MGC:13853 IMAGE:4212293" /lssue_type="Liver, normal, 5 month old male mouse." /clone_id="NCI_CGAP_L19" /lab_host="DH10B" /note="vector: pcMV-SPORT6" 2. .4108 /gene="Sgpl1" /note="synonym: DIORf456" /db_xref="LocustID:20397" /db_xref="MGJ:1261415" 137. 1843 /codon_start=1 /product="sphingosine phosphate lyase 1" /protein_id="AAH26135.1" /db_xref="GI:20072151" /db_xref="LOCUSTID:20397" /translaton="MECTDLTKDKDEPEYLLSYSTAKNVNYNGCYEPBMOLIA WSYLCTLITVMVELLPQPSLSRSRRKKLFKLIRKMPLFGRIIEBOVSARKADLVKN MPFLKLDKVIVKTLPAGWGMTAVLELUKLTSSMDSDWOGSKASGVANYNEPYTLIEL VOAYGEFTSNPLPHDPFIQLRKILEVIWTCSLFNGPGDSOCVTSGGTESIIALL KARDALELGICTPTEIPVAESPAAHFDRKAHYEGMKIYVALVKNNVEDOVAMKRAI

source 1.1707 /organism="unknown"
 BASE COUNT 460 a 376 c 440 g 431 t
 ORIGIN

Query Match 74.9%; Score 1278.2; DB 6; Length 1707;
 Best Local Similarity 84.3%; Pred. No. 0;
 Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

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 VERSION AR267064.1 GI:29696646
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1707)
 AUTHORS Saba,J.D. and Zhou,J.
 TITLE Splingosine-1-phosphate lyase polypeptides, polynucleotides and
 modulating agents and methods of use therefor
 PATENT: US 6495359-A 17-DEC-2002;
 JOURNAL Location/Qualifiers
 FEATURES
 source 1.1707
 BASE COUNT 460 a 376 c 440 g 431 t
 ORIGIN

Query Match 74.9%; Score 1278.2; DB 6; Length 1707;
Best Local Similarity 84.3%; Pred. No. 0;
Matches 1439; Conservative 0; Mismatches 268; Indels 0; Gaps 0;

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DEFINITION
Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor.
ACCESSION
BD081353
VERSION
BD081353.1 GI:22626956
KEYWORDS
JP 2001518303-A/1.
SOURCE
unidentified
ORGANISM
unclassified.
REFERENCE
1 (bases 1 to 1707)
Saba,J.D. and Zhou,J.
Sphingosine-1-phosphate lyase polypeptides, polynucleotides and
modulating agents and methods of use therefor
Patent: JP 2001518303-A 1 16-OCT-2001;
CHILDREN'S HOSPITAL MEDICAL CENTER OF NORTHERN CALIFORNIA
OS Unidentified
PN JP 2001518303-A/1
PD 16-OCT-2001
PF 29-SEP-1998 JP 2000513957
PR 29-SEP-1997 US 08/938309
PI JULIE D SABA,JIANHUI ZHOU
PC C12M15/09,A01K67/027,A61K31/711,A61K38/51,A61K39/395,A61K39/

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1699	99.5	2130	20	AAZ06342	Sphingosine-1-phos
4	1699	99.5	2446	22	AAK51594	Human polynucleoti
5	1697.4	99.4	2093	22	AAK52578	Human polynucleoti
6	1278.2	74.9	1707	20	AAK25366	Mouse sphingosine-
7	1217	71.3	1467	20	AAK25570	Human altered sph
8	401.6	23.5	1746	23	ABL14565	Drosophila melanog

9	401.6	23.5	1782	23	ABL14555	Drosophila melanog
10	401.6	23.5	2060	22	AAD06842	Drosophila melanog
11	284.4	16.7	785	20	AAZ06343	Sphingosine-1-phos
12	256.2	15.0	1770	20	AAK25569	Yeast sphingosine-
13	256.2	15.0	2270	22	AAH29742	S cerevisiae apopt
14	225.6	13.2	1629	20	AAK25568	C. elegans sphingo
15	224.4	13.1	4937	23	ABL14554	Drosophila melanog
16	224.4	13.1	5187	23	ABL14564	Drosophila melanog
17	208.2	12.2	1670	21	AAK07526	Fusarium venenatum
18	194.2	11.4	2270	21	AAH29885	C albicans apoptos
19	182.4	10.7	665	22	AAH08446	Human CDNA clone (
20	182.4	10.7	2955	22	AAH18267	Human CDNA sequenc
21	148	8.7	1092	25	ABK52445	Aspergillus oryzae
22	116.4	6.8	293	21	AAK16916	Human secreted pro
23	72.4	4.2	531	21	AAK40024	Arabidopsis thalia
24	63.8	3.7	349980	22	AAK41225	Pyrococcus abyssi
25	58.4	3.4	60	24	ABK37114	Human spliced tran
26	50.8	3.0	393	22	AAH50937	Lipid degradation
27	50.8	3.0	393	22	AAH56944	P patens lipid met
28	48.6	2.8	4590	22	AAH24065	Yeast AOD9604-asso
29	39.2	2.3	1830	23	AAH81857	CDNA encoding novel
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31	37.8	2.2	3576	25	ABK75047	Human kielin-like
32	37.8	2.2	3621	25	ABK75048	Human kielin-like
33	37.8	2.2	4431	25	ABK75042	Human kielin-like
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36	37.6	2.2	1268	18	AAK74604	Staphylococcus aur
37	37.6	2.2	1835	23	AAH89928	DNA encoding novel
38	37.6	2.2	2503	20	AAK28272	S. aureus p1A cod
39	36.8	2.2	1870	21	AAK33165	Arabidopsis thalia
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41	36.2	2.1	294	23	ABV30204	Human prostate exp
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43	36.2	2.1	471	23	ABV45707	Human prostate exp
44	36.2	2.1	2277	25	ABK75049	Human kielin-like
45	36.2	2.1	3173	25	ABK75041	Human kielin-like

ALIGNMENTS

RESULT 1	
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ID	AAK25567 standard; CDNA; 1707 BP.
AC	AAK25567;
XX	
DT	02-AUG-1999 (first entry)
XX	
DE	Human sphingosine-1-phosphate lyase CDNA.
XX	
KW	Sphingosine-1-phosphate lyase; SPL; human; breast cancer;
KW	diagnosis; prognosis; therapy; ss.
XX	
OS	Homo sapiens.
XX	
PN	W03916888-A2.
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PD	08-APR-1999.
XX	
PF	29-SEP-1998; 98WO-US20365.
XX	
PR	29-SEP-1997; 97US-0939309.
XX	
PA	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
PI	Saba JD, Zhou J;
XX	
XX	WPI: 1999-263700/22.
DR	P-PSDB; AAY05827.
XX	
PT	Sphingosine-1-phosphate lyase, polynucleotides and modulators

XX Claim 1: Page 68-72; 96pp; English.
PS This is the nucleotide sequence of human cDNA coding for
CC sphingosine-1-phosphatase (SPL, see AY05827). SPL cDNA was
CC obtained by amplification of human fibroblast RNA. SPL
CC catalyzes the cleavage of sphingosine-1-phosphate into inactive
CC metabolites. Sphingosine-1-phosphate is an endogenous tumour
CC suppressor lipid that potentially inhibits breast cancer cell growth
CC and invasiveness, while not affecting the growth of non-tumour
CC cells. Mouse and human SPL polynucleotides (see AX25666-67) and
CC polypeptides (see AY05826-29) are claimed. Methods are provided for
CC preparing SPL using transformed or transfected host cells. SPL
CC polypeptides are used in claimed methods for identifying agents that
CC modulate SPL activity. SPL inhibitors will inhibit growth of cancer
CC cells, especially breast cancer cells. SPL inhibitors, including
CC polynucleotides preventing expression of SPL genes, or antibodies
CC against SPL, can also be used to prevent the development and/or
CC metastasis of cancer, especially where the inhibitor is linked to
CC an antitumour or antioestrogen receptor antibody. Detection of
CC alterations in an endogenous SPL sequence, especially where the
CC alteration is a deletion of residues 354-433 of the 568 amino acid
CC human SPL sequence (see also AY05830), can be used to diagnose
CC cancer, and to assess the prognosis for recovery.
XX
SQ Sequence 1707 BP; 467 A; 388 C; 424 G; 428 T; 0 other;
Query Match 100.0%; Score 1707; DB 20; Length 1707;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCTACGACGACGACCTCTGATGTTGAAGGCTTTGAGCCCTACTAGAGATTTTGA
1 ATGCTACGACGACGACCTCTGATGTTGAAGGCTTTGAGCCCTACTAGAGATTTTGA
61 GATATCTCCACAAAGCCAGATATGTAATGACATGACCAAGATATGACCCCTGG
61 GATATCTCCACAAAGCCAGATATGTAATGACATGACCAAGATATGACCCCTGG
121 CAGTAAATTCATGAGAGTGTGTCGACCCCTGCTGATAGTGGGATGATGTTTGC
121 CAGTAAATTCATGAGAGTGTGTCGACCCCTGCTGATAGTGGGATGATGTTTGC
181 TTCACGCCAGAGATTTATGTCAGAGTTTAAAAAGATTTTAAAGCTCCAGAGAG
181 TTCACGCCAGAGATTTATGTCAGAGTTTAAAAAGATTTTAAAGCTCCAGAGAG
241 ATGCCATTATGTCGTAAGATTCAGACAGTTGAACAGCAAGAGATGATTTAGC
241 ATGCCATTATGTCGTAAGATTCAGACAGTTGAACAGCAAGAGATGATTTAGC
301 AAGACATGTCATTCCTGTAAGAGTGAAGATGTAAGAGTTTACCTCCAGAGGT
301 AAGACATGTCATTCCTGTAAGAGTGAAGATGTAAGAGTTTACCTCCAGAGGT
361 CTGACACTATCTGCTGTTTGGAGAACTTAAGAGTACGCTATGAGACCCCTTGG
361 CTGACACTATCTGCTGTTTGGAGAACTTAAGAGTACGCTATGAGACCCCTTGG
421 CAAGAGGGAGAGCCTCTGGAACAGTACAGTGGGAGAGAGAACCTCAGAGCTCT
421 CAAGAGGGAGAGCCTCTGGAACAGTACAGTGGGAGAGAGAACCTCAGAGCTCT
481 GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGCAATGATCTTCCACAGA
481 GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGCAATGATCTTCCACAGA
541 CTACCAAGATGAGAGCAAGAAATGTGAGATAGCTTGTCCCTTTCAATGGGGACCA
541 CTACCAAGATGAGAGCAAGAAATGTGAGATAGCTTGTCCCTTTCAATGGGGACCA
601 GATTGCTGATGTCATCTCTGAGGAGAGAGAAACATGATGCTGCTGCAAAACA
601 GATTGCTGATGTCATCTCTGAGGAGAGAGAAACATGATGCTGCTGCAAAACA

601 GATTGCTGATGTCATCTCTGAGGAGAGAGAAACATGATGCTGCTGCAAAACA 660
661 TGTCCGATCTGGCCCTTTGAGAGGGATCAAAACTCCAGAAATGTGGCTCCCAAGT
661 TGTCCGATCTGGCCCTTTGAGAGGGATCAAAACTCCAGAAATGTGGCTCCCAAGT
721 GGCATGCTGATTTAACAAAGCAGCTTACTTTGGATGAGATTTGGGGTCCCA
721 GGCATGCTGATTTAACAAAGCAGCTTACTTTGGATGAGATTTGGGGTCCCA
781 TTAGCAAGATGATGAGAGTGGATGAGGGCAATGAGAGAGATATCCAGAACT
781 TTAGCAAGATGATGAGAGTGGATGAGGGCAATGAGAGAGATATCCAGAACT
840 TTAGCAAGATGATGAGAGTGGATGAGGGCAATGAGAGAGATATCCAGAACT
840 TTAGCAAGATGATGAGAGTGGATGAGGGCAATGAGAGAGATATCCAGAACT
900 GGCATGCTGATTTAACAAAGCAGCTTACTTTGGATGAGATTTGGGGTCCCA
900 GGCATGCTGATTTAACAAAGCAGCTTACTTTGGATGAGATTTGGGGTCCCA
960 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCAATGTCAGAGCTTGT
960 GTGGCCAAAGCTGGCTGTCAAAATACAAATACCCCTTCAATGTCAGAGCTTGT
1020 TTTCTCATGCTTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1020 TTTCTCATGCTTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1080 GTGAAGGCTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1080 GTGAAGGCTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1140 TCATATGCTGCTTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1140 TCATATGCTGCTTTATGAGAGAAAGCAGATACCCAGTGAAGCAGCATTGATTCGG
1200 GATTGGAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1200 GATTGGAGGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1260 AGCGAGGCTGTGGGCTGCTTGTGATGACCTTGGTGAAGAGGCTATGTTGAAGTAC
1260 AGCGAGGCTGTGGGCTGCTTGTGATGACCTTGGTGAAGAGGCTATGTTGAAGTAC
1320 AAACGATCATCAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1320 AAACGATCATCAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1380 TTTGTTTGGGAATCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1380 TTTGTTTGGGAATCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1440 TACGACATCAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1440 TACGACATCAAAACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1500 CCCAGTATCAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1500 CCCAGTATCAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1560 CTAAGAGCATTCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1560 CTAAGAGCATTCGAGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
1620 GGAATGGTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1620 GGAATGGTGCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT
1680 TTTGCTCAGTCTTTTGGAGAGCTTGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
1680 TTTGCTCAGTCTTTTGGAGAGCTTGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
1740 ATGAATGGTCTCCAAACCCCACTGA 1707
1740 ATGAATGGTCTCCAAACCCCACTGA 1707

RESULT 2
ID ABL59529 standard; cDNA: 1707 BP.
XX ABL59529;
XX
XX 16-JUL-2002 (first entry)
XX
XX Human sphingosine-1-phosphate lyase 1 cDNA SEQ ID NO:29.
XX
XX Human; sphingosine-1-phosphate lyase 1; enzyme;
XX tumour; lipid associated gene; lipid metabolism; lipid synthesis;
XX chromosome 10q21; gene; ss.
XX
XX Homo sapiens.
XX
XX WO200227028-A1.
XX
XX 04-APR-2002.
XX
XX 27-SEP-2001; 2001WO-US0366.
XX
XX 28-SEP-2000; 2000US-0676052.
XX
XX (ATAI-) AFAIRGIN TECHNOLOGIES INC.
XX
XX Skinner MK, Patton JL, Chaudhary J;
XX
XX WPI; 2002-402054/43.
XX
XX Identifying tumor characteristics in a tissue sample taken from a
XX patient, involves determining the copy number or expression level of
XX genes associated with lipid metabolism, synthesis or action
XX
XX Example 1; Page 87; 113pp; English.
XX
XX The present invention describes a method for identifying tumour
XX characteristics, comprising measuring a copy number or expression level
XX of at least two genes associated with lipid metabolism, synthesis, or
XX action in cells from a patient tissue sample, and comparing the results
XX with a copy number or expression level of the genes in a normal cell.
XX Also described is an array of nucleic acid polymers immobilised on a
XX solid support, comprising a solid support, at least two different nucleic
XX acid polymers which are each specific for a different gene associated
XX with lipid metabolism, synthesis or action, where each nucleic acid
XX polymer is located at a predetermined position on the solid support, and
XX the array comprises nucleic acid polymers which are specific for less
XX than 100 genes other than the selected genes. The method is useful for
XX determining tumour characteristics in a tissue sample taken from a
XX patient. The present sequence represents a human lipid-associated gene
XX related cDNA sequence, which is used in the exemplification of the
XX present invention.
XX
XX Sequence 1707 BP; 468 A; 386 C; 425 G; 428 T; 0 other;
XX
XX
XX Query Match 99.7%; Score 1702.2; DB 24; Length 1707;
XX Best Local Similarity 99.8%; Pred. No. 0;
XX Matches 1704; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

181 TTCCAGCAGAGAGTTATGCTCAAGCTTTAAAGAAATGTTTAAAGCTCAGCAGAG 240
181 TTCCAGCAGAGAGTTATGCTCAAGCTTTAAAGAAATGTTTAAAGCTCAGCAGAG 240
241 ATGCCCATTTATGCTGCTAGATTCAGACAGAGTTGAACAAGCCAAAGATGATTTAGC 300
241 ATGCCCATTTATGCTGCTAGATTCAGACAGAGTTGAACAAGCCAAAGATGATTTAGC 300
301 AAGAACATGTCATTCCTGAAAGTGGACAAAGATGTAAGAACTTTACCTCCAGAGGT 360
301 AAGAACATGTCATTCCTGAAAGTGGACAAAGATGTAAGAACTTTACCTCCAGAGGT 360
361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACAGCTTATGAGAGCCTTCGG 420
361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGATACAGCTTATGAGAGCCTTCGG 420
421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAAAGCTCAGCTCCTT 480
421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGGAGAGAAAGCTCAGCTCCTT 480
481 GTGAAGGCTTATGAGAGATTTTGCATGAGTAAACCCCTGCAATCCAGATATCTCCAGGA 540
481 GTGAAGGCTTATGAGAGATTTTGCATGAGTAAACCCCTGCAATCCAGATATCTCCAGGA 540
541 CTACGCAAGATAGAGGAGAAATTTGAGATAGCTTGTCCCTGTTCAATGGGGAGACA 600
541 CTACGCAAGATAGAGGAGAAATTTGAGATAGCTTGTCCCTGTTCAATGGGGAGACA 600
601 GATTGCTGTGATGTGACTTCTGGGGGAAACAGAAAGCATATCATGAGCCTGCAAGACA 660
601 GATTGCTGTGATGTGACTTCTGGGGGAAACAGAAAGCATATCATGAGCCTGCAAGACA 660
661 TGTGGGATCTGCGCTTTGAGAAAGGGATCAAACTCCAGAAATTTGGCTCCCAAGT 720
661 TGTGGGATCTGCGCTTTGAGAAAGGGATCAAACTCCAGAAATTTGGCTCCCAAGT 720
721 GCCCATGCTGATTTAAACAAAGCAGCAGTACTTTGGAGTGAAGATGTGCGGGTCCA 780
721 GCCCATGCTGATTTAAACAAAGCAGCAGTACTTTGGAGTGAAGATGTGCGGGTCCA 780
781 TTGACGAAGATGATGAGAGTGTGATGAGGGCAATGAAAGAGCTATCTCCAGAAACT 840
781 TTGACGAAGATGATGAGAGTGTGATGAGGGCAATGAAAGAGCTATCTCCAGAAACT 840
841 GCCATGCTGCTGCTTTTACCCACAGTTCCTCATGCTGTAATGATCTGCTCCGAA 900
841 GCCATGCTGCTGCTTTTACCCACAGTTCCTCATGCTGTAATGATCTGCTCCGAA 900
901 GTGGCCAAAGCTGCTGTCAAATACCAATACCCCTTCATGTCGACGCTTGTGGAGGC 960
901 GTGGCCAAAGCTGCTGTCAAATACCAATACCCCTTCATGTCGACGCTTGTGGAGGC 960
961 TTCCTCATCTGCTTTATGAGAAAGCAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
961 TTCCTCATCTGCTTTATGAGAAAGCAGAGATACCCACTGAGACACCATTTGATTTCCGG 1020
1021 GTGAAGGTGTAACACACATTTACGTCGACACCCCATTAAGTATGCTATGCCCCAAAGGC 1080
1021 GTGAAGGTGTAACACACATTTACGTCGACACCCCATTAAGTATGCTATGCCCCAAAGGC 1080
1081 TCATCATTTGCTGTTATGAGCAACAAGATACAGAACTATCATGTTCTTCTGCTGATACA 1140
1081 TCATCATTTGCTGTTATGAGCAACAAGATACAGAACTATCATGTTCTTCTGCTGATACA 1140
1141 GATTGGAGGGTGGCATCTATGCTTCCCAACATTCAGAGGCTCAGGCTGATGCAATT 1200
1141 GATTGGAGGGTGGCATCTATGCTTCCCAACATTCAGAGGCTCAGGCTGATGCAATT 1200
1201 AGCGCAGCCTGTTGGGCTGCTGATGACATCTTGGTGAAGAGGCTATGTTGAAGCTACC 1260
1201 AGCGCAGCCTGTTGGGCTGCTGATGACATCTTGGTGAAGAGGCTATGTTGAAGCTACC 1260
1261 AACACAGATCATCAAAACTGCTGCTCCTCAAGTCAAGACTGCAAAATATCAAGGATC 1320

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DB      1261  |||||||
OY      1321  |||||||
DB      1321  |||||||
OY      1381  |||||||
DB      1381  |||||||
OY      1381  |||||||
DB      1381  |||||||
OY      1441  |||||||
DB      1441  |||||||
OY      1501  |||||||
DB      1501  |||||||
OY      1561  |||||||
DB      1561  |||||||
OY      1621  |||||||
DB      1621  |||||||
OY      1681  |||||||
DB      1681  |||||||

RESULT 3
AA206342
ID      AA206342 standard; DNA; 2130 BP.
XX      AA206342;
XX      26-OCT-1999 (first entry)
DE      Sphingosine-1-phosphate lyase nucleotide sequence.
XX      sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
XX      G-protein coupled receptor; EDS-1; secondary messenger; cancer;
XX      cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
XX      stroke; apoptosis; ds.
OS      Homo sapiens.
XX      Homo sapiens.
XX      Key      location/Qualifiers
XX      CDS      178..1384
XX      FT      /tag= a
XX      FT      /product= "Sphingosine-1-phosphate lyase"
XX      W09938983-A1.
XX      PD      05-AUG-1999.
XX      PF      24-DEC-1998; 98WO-EP08564.
XX      PR      03-NOV-1998; 98GB-0024026.
XX      PR      29-JAN-1998; 98BP-0300625.
XX      PA      (SMK ) SMITHKLINE BEECHAM PLC.
XX      PI      Duckworth DM, Godden RJ, Testa TT;
XX      DR      WPI: 1999-479192/40.
XX      DR      P-PSDB: AA115211.
XX      PT      A new sphingosine-1-phosphate lyase useful for diagnosing and
XX      PT      treating cancers, cardiovascular disorders, thrombosis or
XX      PT      atherosclerosis

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XX      Claim 7; Page 23; 37pp; English.
PS      This is the nucleotide sequence of Sphingosine-1-phosphate lyase. The
XX      CC      lyase catalyses the cleavage of Sphingosine-1-phosphate to give a long
XX      CC      chain aldehyde and phosphoethanolamine.
XX      CC      The sequence can form the basis of a method of treating cancers, cardiac
XX      CC      disorders, thrombosis, atherosclerosis and other conditions. This is due
XX      CC      to the action of Sphingosine-1-phosphate intracellularly as a secondary
XX      CC      messenger and extracellularly as a ligand for the G-protein coupled
XX      CC      receptor EDG-1.
XX      Sequence 2130 BP; 563 A; 479 C; 561 G; 527 T; 0 other.
XX      Query Match      99.5%; Score 1699; DB 20; Length 2130;
XX      Best Local Similarity 99.7%; Pred. No. 0;
XX      Matches 1702; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY      1  ATGCTAGCAGACACCTTGTATGTTGAAGCCCTTGAGCCCTACTAGATTTTGGAA 60
DB      178  ATGCTAGCAGACACCTTGTATGTTGAAGCCCTTGAGCCCTACTAGATTTTGGAA 237
OY      61  GTATACCTCCAAAGGCCAAGAAATTATGTAATGGACATTTGACCAAGATAGGCCCTGG 120
DB      238  GTATACCTCCAAAGGCCAAGAAATTATGTAATGGACATTTGACCAAGATAGGCCCTGG 297
OY      121  CAGCTAATTGCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGATTGTTC 180
DB      298  CAGCTAATTGCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGATTGTTC 357
OY      181  TTCCAGCCAGAGAGTTTATGTCAAAGTTTAAAAAGTTTAAAGTTTAAAGTTTAAAGTTT 240
DB      358  TTCCAGCCAGAGAGTTTATGTCAAAGTTTAAAAAGTTTAAAGTTTAAAGTTTAAAGTTT 417
OY      241  ATGCCCATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 300
DB      418  ATGCCCATTTATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 477
OY      301  AAGAACATGTCATTCCTGTAAGTGAACAAGATATGTAAGTGAACAAGATATTCCTGTAAG 360
DB      478  AAGAACATGTCATTCCTGTAAGTGAACAAGATATGTAAGTGAACAAGATATTCCTGTAAG 537
OY      361  CTGAGCTATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTATAGGAGCCCTTCTGG 420
DB      538  CTGAGCTATCTGCTGTTTGGAGAACTTAAGAGTACAGTCTATAGGAGCCCTTCTGG 597
OY      421  CAAGAGGGAGAGCCCTGGAACAGTGTACAGTGTGGAGGAGAGAGAGTCACTAGCTCTT 480
DB      598  CAAGAGGGAGAGCCCTGGAACAGTGTACAGTGTGGAGGAGAGAGAGTCACTAGCTCTT 657
OY      481  GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGTCATCAGATATCTTCCAGGA 540
DB      658  GTGAAGGCTTATGAGATTTTGCATGAGTAACCCCTGTCATCAGATATCTTCCAGGA 717
OY      541  CTAGCAGATGAGAGCAAGAAATTGTGAGATAGCTTGTCCCTGTAAGGGGAGACA 600
DB      718  CTAGCAGATGAGAGCAAGAAATTGTGAGATAGCTTGTCCCTGTAAGGGGAGACA 777
OY      601  GATTGCTGATGTGTGACTTCTGGGGAAACAGAAACATCTCATGAGCCCTGCAAAACA 660
DB      778  GATTGCTGATGTGTGACTTCTGGGGAAACAGAAACATCTCATGAGCCCTGCAAAACA 837
OY      661  TGTGGGATCTGGCCCTTGGAGAGGGATCAAAACTCCAGAAATTTGGCTCCCAAGT 720
DB      838  TATCGGATCTGGCCCTTGGAGAGGGATCAAAACTCCAGAAATTTGGCTCCCAAGT 897
OY      721  GCCCATGCTGATTTAACAAGACAGCACTTACTTTGGAGTGAAGATTTGGGGTCCCA 780
DB      898  GCCCATGCTGATTTAACAAGACAGCACTTACTTTGGAGTGAAGATTTGGGGTCCCA 957
OY      781  TTGACGAAGATGATGAGTGTGATGTGAGGCAATGAGAAGAGTATCTCCAGAAACT 840
DB      958  TTGACGAAGATGATGAGTGTGATGTGAGGCAATGAGAAGAGTATCTCCAGAAACT 1017

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Db 440 ATGCCATTTATTTGTCGTAGATTCAAGCAAGTTGAACAAACCAAGATATATATTAC 499
Oy 301 AAGAACATGTCATTTCTCTGAAGTGGACAAAGATATGTAAGCTTTACCTCCAGGT 360
Db 500 AAGAACATGTCATTTCTCTGAAGTGGACAAAGATATGTAAGCTTTACCTCCAGGT 559
Oy 361 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGGAGCCCTTGG 420
Db 560 CTGAGCTCATCTGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGGAGCCCTTGG 619
Oy 421 CAAGAGGGAGAGCCCTGAGACAGTGTACGTGGGAGAGAGAGTCACTGAGCTCTT 480
Db 620 CAAGAGGGAGAGCCCTGAGACAGTGTACGTGGGAGAGAGAGTCACTGAGCTCTT 679
Oy 481 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATATCTTCCAGA 540
Db 680 GTGAAGGCTTATGAGATTTTGCATGAGTAAACCCCTGCATCCAGATATCTTCCAGA 739
Oy 541 CTACGCAGATGAGAGGCAAAATTTGTAGAGTACCTTCTCCCTGTTCAATGGGGACCA 600
Db 740 CTACGCAGATGAGAGGCAAAATTTGTAGAGTACCTTCTCCCTGTTCAATGGGGACCA 799
Oy 601 GATTGCTGATGATGTGACTCTGGGGAGACAGAAAGCATCTGATGGCCCTGCAAGA 660
Db 800 GATTGCTGATGATGTGACTCTGGGGAGACAGAAAGCATCTGATGGCCCTGCAAGA 859
Oy 661 TGTGGGATCTGGCCCTTGAAGGGGATCAAAACCTCCAGAAATTTGGGCTCCCAAGT 720
Db 860 TATCGGAGATCTGGCCCTTGAAGGGGATCAAAACCTCCAGAAATTTGGGCTCCCAAGT 919
Oy 721 GCCCATGCTGCAATTAACAAAGCAGCAGTACTTTGGATGAAGTTGTCGGGTCCA 780
Db 920 GCCCATGCTGCAATTAACAAAGCAGCAGTACTTTGGATGAAGTTGTCGGGTCCA 979
Oy 781 TTGACGAAGATGATGAGGTGATGAGGGCAATGAGAAGAGTATCTCCAGGAACCT 840
Db 980 TTGACGAAGATGATGAGGTGATGAGGGCAATGAGAAGAGTATCTCCAGGAACCT 1039
Oy 841 GCCATGCTGCTGTTCTTAACCCACAGTTTCTCAATGTTAATAGATCTGTCCTGAA 900
Db 1040 GCCATGCTGCTGTTCTTAACCCACAGTTTCTCAATGTTAATAGATCTGTCCTGAA 1099
Oy 901 GTGGCCAGCTGCTGCTCAATTAACAAATACCCCTTCAATGTCAGCGCTTGTGGAGGC 960
Db 1100 GTGGCCAGCTGCTGCTCAATTAACAAATACCCCTTCAATGTCAGCGCTTGTGGAGGC 1159
Oy 961 TTCTCATGCTGCTTATGAGAGAAAGCAGATACCCACAGGAGCACCATTGATTTCGG 1020
Db 1160 TTCTCATGCTGCTTATGAGAGAAAGCAGATACCCACAGGAGCACCATTGATTTCGG 1219
Oy 1021 GTGAAGGTGTAAACAGCATTTACAGTACACCCATTAATGCTATGCCCAAAAGC 1080
Db 1220 GTGAAGGTGTAAACAGCATTTACAGTACACCCATTAATGCTATGCCCAAAAGC 1279
Oy 1081 TCATCATGCTGCTTATGAGAGAAAGTACAGAACTATCACTTCTGTCGATACA 1140
Db 1280 TCATCATGCTGCTTATGAGAGAAAGTACAGAACTATCACTTCTGTCGATACA 1339
Oy 1141 GATTGGCAGGTGATCATCTATGCTCCCAACCATCGAGGTGACGGCTGGTGGCAAT 1200
Db 1340 GATTGGCAGGTGATCATCTATGCTCCCAACCATCGAGGTGACGGCTGGTGGCAAT 1399
Oy 1201 AGCGAGGCTGTTGGGCTGCTTGAAGCACTTGGTGAAGCGCTATGTTGAAGCTACC 1260
Db 1400 AGCGAGGCTGTTGGGCTGCTTGAAGCACTTGGTGAAGCGCTATGTTGAAGCTACC 1459
Oy 1261 AAACGATCATCAAAAGCTGCTGCTCTCAAGTACAGACTGGAATAATCAAGGACATC 1320
Db 1460 AAACGATCATCAAAAGCTGCTGCTCTCAAGTACAGACTGGAATAATCAAGGACATC 1519
Oy 1321 TTTGTTTTGGGAATCCCAATGTGCACTCAATGCTCGGAGATCCCGGATTTTGACATC 1380
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
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Db 1520 TTTGTTTTGGGAATCCCAATGTGCACTCAATGCTCTGGGATCCCGTGAATTTTGACATC 1579
Oy 1381 TACCGCATATCAAAACCTGATGACTGTAAGGGGTGGAACCTTAACAGTTCAGTCCCA 1440
Db 1580 TACCGCATATCAAAACCTGATGACTGTAAGGGGTGGAACCTTAACAGTTCAGTCCCA 1639
Oy 1441 CCCAGTATTCATTTCTGATCAATTAACATTAACAGCCCGGAACAGTACTATACATTC 1500
Db 1640 CCCAGTATTCATTTCTGATCAATTAACATTAACAGCCCGGAACAGTACTATACATTC 1699
Oy 1501 CTAAAGGACATTCGAAATCTGCACTCAATCAATGAAGAAATCTAAAGCGAAGCCCA 1560
Db 1700 CTAAAGGACATTCGAAATCTGCACTCAATCAATGAAGAAATCTAAAGCGAAGCCCA 1759
Oy 1561 GGAATGGGTGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1620
Db 1760 GGAATGGGTGATCATATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1819
Oy 1621 TTTGCTCTAGTCTTCTTGGACAGCTTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1680
Db 1820 TTTGCTCTAGTCTTCTTGGACAGCTTTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1879
Oy 1681 ATGAATGGTTCTCCAAACCCCACTGA 1707
Db 1880 ATGAATGGTTCTCCAAACCCCACTGA 1906
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RESULT 5

AAK52578 ID AAK52578 standard; cDNA; 2093 BP.

AAK52578;

06-NOV-2001 (first entry)

Human polynucleotide SEQ ID NO 2107.

Human; cytokine; cell proliferation; cell differentiation; gene therapy;

KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;

KW tissue growth factor; immunomodulatory; cancer; leukaemia;

KW nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

PA (HSE-) HYSEQ INC.

Tang YT, Liu C, Dimaenac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y, Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW, Xue AJ, Yang Y, Wejhrman T, Goodrich R;

WPI: 2001-476283/51.

P-PSDB; AAM79445.

Nucleic acids encoding polypeptides with cytokine-like activities,

useful in diagnosis and gene therapy -

Claim 1; Page 4485; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK80323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoietic regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK8020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.

XX Sequence 2093 BP; 565 A; 465 C; 539 G; 524 T; 0 other;

Query Match 99.4%; Score 1697.4; DB 22; Length 2093;

Best Local Similarity 99.6%; Pred. No. 0;

Matches 1701; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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QY 1 AAGCCTAGCAGACACCTTGTGATGTTGAAGCCCTTGAAGCCTTGAAGATTTTGAA 60
DB 133 ATGCCCTAGCAGACACCTTGTGATGTTGAAGCCCTTGAAGCCTTGAAGATTTTGAA 192
QY 61 GTATCTCCCAAAAAGCAGAAATTTGTAATGACATTTGACCAAGATATGAGCCCTGG 120
DB 193 GTATCTCCCAAAAAGCAGAAATTTGTAATGACATTTGACCAAGATATGAGCCCTGG 252
QY 121 CAGCTAATTCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGAGTTGTC 180
DB 253 CAGCTAATTCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGAGTTGTC 312
QY 181 TTCCAGCCAGAGGTTTATGCTCAAGTTTAAAAAATGTTTAAAGTCAACAGAGAG 240
DB 313 TTCCAGCCAGAGGTTTATGCTCAAGTTTAAAAAATGTTTAAAGTCAACAGAGAG 372
QY 241 ATGCCCTAATTCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGAGTTGTC 300
DB 373 ATGCCCTAATTCATGAGTGTCTGTGACCCCTGCTGATAGTCTGGGATATGAGTTGTC 432
QY 301 AAGAACATGTCATTCCTGAAAGTGACAAAGATATGTAAGCTTACCTCCAGGGT 360
DB 433 AAGAACATGTCATTCCTGAAAGTGACAAAGATATGTAAGCTTACCTCCAGGGT 492
QY 361 CTGAGCTCATTCGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGACGCTTCTGG 420
DB 493 CTGAGCTCATTCGCTGTTTGGAGAACTTAAGAGTACAGCTCTATGACGCTTCTGG 552
QY 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTGAGCTCTT 480
DB 553 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAGAGCTCACTGAGCTCTT 612
QY 481 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCCAGATATCTTCCAGGA 540
DB 613 GTGAAGGCTTATGAGATTTTGCATGAGATTAACCCCTGATCCAGATATCTTCCAGGA 672
QY 541 CTACGCAATATAGAGCAGAAATTTGAGAGTATGCTTCTCTGTTCAATGGGGACCA 600
DB 673 CTACGCAATATAGAGCAGAAATTTGAGAGTATGCTTCTCTGTTCAATGGGGACCA 732
QY 601 GATTCTGTGATGATGCTTGTGGGGAACAGAAAGCACTACTCATGGGCTCCAAAGCA 660
DB 733 GATTCTGTGATGATGCTTGTGGGGAACAGAAAGCACTACTCATGGGCTCCAAAGCA 792
QY 661 TGTGGGATCTGGCCTTTGAGAAAGGGGATCAAAATCTCAGAAATTTGCTCCCAAGT 720
DB 793 TATCGGATCTGGCCTTTGAGAAAGGGGATCAAAATCTCAGAAATTTGCTCCCAAGT 852
QY 721 GCCCATGCTGATTTTAAAGAGCAGCTTACTTTGGGATGAAATTTGGCGGGTCCCA 780
DB 853 GCCCATGCTGATTTTAAAGAGCAGCTTACTTTGGGATGAAATTTGGCGGGTCCCA 912
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QY 781 TTGACGAAGATGATGAGGATGATGATGAGGCAATGAGAAGACTATCTCCAGAACT 840
DB 913 TTGACGAAGATGATGAGGATGATGATGAGGCAATGAGAAGACTATCTCCAGAACT 972
QY 841 GCCATGCTGCTGTTTCTACCCACAGTTTCTCATGATGTTAATAGATCTGCTCGAA 900
DB 973 GCATGCTGCTGTTTCTACCCACAGTTTCTCATGATGTTAATAGATCTGCTCGAA 1032
QY 901 GTGGCCAACTGGCTGTCAATATCAAAATATCCCTTCATGCTGACGCTTGTGGAGGC 960
DB 1033 GTGGCCAACTGGCTGTCAATATCAAAATATCCCTTCATGCTGACGCTTGTGGAGGC 1092
QY 961 TTCCCTATGCTGCTTATGGAAGAGAGATACCACTGAGAGCACCATTGATTCGG 1020
DB 1093 TTCCCTATGCTGCTTATGGAAGAGAGATACCACTGAGAGCACCATTGATTCGG 1152
QY 1021 GTGAAGGTTGTAACAGCATTTTCAAGTGAACCCATTAATAGCTATGCCCCAAAGGC 1080
DB 1153 GTGAAGGTTGTAACAGCATTTTCAAGTGAACCCATTAATAGCTATGCCCCAAAGGC 1212
QY 1081 TCATCATTTGCTGTTGATAGTGAACAAGATGACAGAACTATGATTTCTGCTGATACA 1140
DB 1213 TCATCATTTGCTGTTGATAGTGAACAAGATGACAGAACTATGATTTCTGCTGATACA 1272
QY 1141 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGACAGGCTCACGGCTGCTGTCATT 1200
DB 1273 GATTGGCAGGGTGGCATCTATGCTTCCCAACCATGACAGGCTCACGGCTGCTGTCATT 1332
QY 1201 AGCGAGCCTGTTGGGCTGCTTGAATGACATTCGTTGAGAGACGGCTATGTTGAAGTACC 1260
DB 1333 AGCGAGCCTGTTGGGCTGCTTGAATGACATTCGTTGAGAGACGGCTATGTTGAAGTACC 1392
QY 1261 AAACAGATCATCAAAACTGCTGCTTCCCAATGCAATGCAAGAACTGGAATAATCAAAAGCATC 1320
DB 1393 AAACAGATCATCAAAACTGCTGCTTCCCAATGCAATGCAAGAACTGGAATAATCAAAAGCATC 1452
QY 1321 TTTGTTTGGGAATCCCAATTTGTCATCTATGCTCTGTGGATCCCGTATTTTGACATC 1380
DB 1453 TTTGTTTGGGAATCCCAATTTGTCATCTATGCTCTGTGGATCCCGTATTTTGACATC 1512
QY 1381 TACGACTATCAAACTGATGACTGCTTAAGGGGTGAACCTTGAACAGATTTGCCA 1440
DB 1513 TACGACTATCAAACTGATGACTGCTTAAGGGGTGAACCTTGAACAGATTTGCCA 1572
QY 1441 CCCAGTATCATTTTTCGATCATCATATACAGCCCGGAAAGAGATGATATCAATTC 1500
DB 1573 CCCAGTATCATTTTTCGATCATCATATACAGCCCGGAAAGAGATGATATCAATTC 1632
QY 1501 CTAAAGACATTTGGAATCTGTCACTCAAAATCATGAAGATCTTAAAGGAGACACA 1560
DB 1633 CTAAAGACATTTGGAATCTGTCACTCAAAATCATGAAGATCTTAAAGGAGACACA 1692
QY 1561 GGAATGGTGCATCTATGCCATGAGCCAGACAACTGTTGACAGAAATATGTTGCAGAA 1620
DB 1693 GGAATGGTGCATCTATGCCATGAGCCAGACAACTGTTGACAGAAATATGTTGCAGAA 1752
QY 1621 TTGCTCTGATCTTCTTGGACAGCTGTACAGACCGAAGCTGCAACCCAGGAGACAG 1680
DB 1753 TTGCTCTGATCTTCTTGGACAGCTGTACAGACCGAAGCTGCAACCCAGGAGACAG 1812
QY 1681 ATGAATGTTCTCAAAACCCCACTGA 1707
DB 1813 ATGAATGTTCTCAAAACCCCACTGA 1839
```

RESULT 6
AAK52566
ID AAK52566 standard; cdna; 1707 BP.

XX AAK52566;

AC AAK52566;

XX

XX

XX

XX

XX

XX

Db 1381 TACGACTATCTATATGATGTCTGTAAGGGTGAATTTTACTACCTGACGTCCCA 1440
 QY 1441 CCCAGTATCTATTTCTGATCACAATCTACAGCCCGGAAACAGTAGCTATCAATTC 1500
 Db 1441 AGAAGCATCTATTTCTGATTAAGTATGATCTAGTACAGGCAAGTGGCATCCAGTTC 1500
 QY 1501 CTAAAGACATTCGAGATCTGTACATCAATCATGAAGATCTTAAAGCAAGCAGCA 1560
 Db 1501 CTAAAGCATATCCGGATCATGTCACACAAATCATGAGATCTTAAAGCTAAAGCCACA 1560
 QY 1561 GGAATGGGTGCTCATCTATGCTGAGCCAGACAACTGTGACAGAAATATGTTGCAAA 1620
 Db 1561 GGAATGGGTGCTCATCTATGCTGAGCCAGACAACTGTGACAGAAATATGTTGCAAA 1620
 QY 1621 TTGTCCTCAGTCTCTGAGACAGTGTGACAGCCAGACACTGTACCCAGGCAAGCAG 1680
 Db 1621 ATATCTCTCCCTCTCTGAGACTGCTTATCTAGGAGACCCGCTGACTCAGAGGCAAGCAG 1680
 QY 1681 ATGATGTTCTCCAAAACCCCACTGA 1707
 Db 1681 ATGATGTTCTCCAAAACCCCGCTGA 1707
 RESULT 7
 ID AAX25570 standard; cDNA: 1467 BP.
 XX AAX25570;
 AC AAX25570;
 D7 02-AUG-1999 (first entry)
 XX Human altered sphingosine-1-phosphate lyase cDNA.
 DE Sphingosine-1-phosphate lyase; SPL; human; breast cancer;
 KM diagnosis; prognosis; therapy; deletion; ss.
 KW Homo sapiens.
 OS
 XX MO9916888-A2.
 PN 08-APR-1999.
 PD 29-SEP-1998; 98WO-US20365.
 PF 29-SEP-1997; 97US-0939309.
 PR (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
 PA Saba JD, Zhou J;
 PI Saba JD, Zhou J;
 DR WPI: 1999-263700/22.
 DR P-PSDB: AAY05830.
 XX Sphingosine-1-phosphate lyase, polynucleotides and modulators
 PT Example 3: Page 90-94; 96pp; English.
 PS
 XX This is the nucleotide sequence of human cDNA coding for altered
 CC sphingosine-1-phosphate lyase (SPL, see AAY05830). The SPL cDNA was
 CC obtained by amplification of human glioblastoma multiforme RNA. The
 CC polypeptide sequence predicted from this SPL cDNA lacks amino acids
 CC 354-433 of SPL predicted from a clone (see AAX25567) obtained from
 CC fibroblast cells. Sphingosine-1-phosphate is an endogenous tumour
 CC suppressor lipid that potentially inhibits breast cancer cell growth
 CC and invasiveness, while not affecting the growth of non-tumour
 CC cells. Detection of alterations in an endogenous SPL sequence,
 CC especially where the alteration is a deletion of residues 354-433
 CC of the 568 amino acid human SPL sequence, can be used to diagnose
 CC cancer, and to assess the prognosis for recovery. Mouse and human
 CC SPL polynucleotides (see AAX25666-67) and polypeptides (see AAY05826-29)
 CC are claimed. The polypeptides are used in claimed methods for
 CC identifying agents that modulate SPL activity. SPL inhibitors will

CC Inhibit growth of cancer cells, especially breast cancer cells.
 CC They can also be used to prevent the development and/or metastasis
 CC of cancer, especially where the inhibitor is linked to an anti-tumour
 CC or anti-estrogen receptor antibody.
 XX
 SO Sequence 1467 BP; 407 A; 328 C; 364 G; 368 T; 0 other;
 Query Match 71.3%; Score 1217; DB 20; Length 1467;
 Best Local Similarity 85.9%; Pred. No. 0;
 Matches 1467; Conservative 0; Mismatches 0; Indels 240; Gaps 1;
 QY 1 ATGCTAGCAGACAGCTTCTGATGTTGAAGCCCTTGAAGCCCTTATGAGATTTTGA 60
 Db 1 ATGCTAGCAGACAGCTTCTGATGTTGAAGCCCTTGAAGCCCTTATGAGATTTTGA 60
 QY 61 GTATATCTCCACAAAAGCCAGAAATATGTAATGACATTTCCACCAAGTATGAGCCCTG 120
 Db 61 GTATATCTCCACAAAAGCCAGAAATATGTAATGACATTTCCACCAAGTATGAGCCCTG 120
 QY 121 CAGCTAATTCATGAGTGTGCTGAGACCTGCTGATGATCTGAGGATATGATTTGTC 180
 Db 121 CAGCTAATTCATGAGTGTGCTGAGACCTGCTGATGATCTGAGGATATGATTTGTC 180
 QY 181 TTCCAGCCAGAGAGTTTATGTCAGAGTTTAAAAAGAAATGTTTAACTCAGCAGAG 240
 Db 181 TTCCAGCCAGAGAGTTTATGTCAGAGTTTAAAAAGAAATGTTTAACTCAGCAGAG 240
 QY 241 ATGCCCATTTATGTCGTTAATATTCAGACAGAGTTGAACAAGCAGCAGAGATTTAGC 300
 Db 241 ATGCCCATTTATGTCGTTAATATTCAGACAGAGTTGAACAAGCAGCAGAGATTTAGC 300
 QY 301 AAGAACATGTCATTCCTGAAGTGAACAGATATGTAAGCTTACCTCCAGAGT 360
 Db 301 AAGAACATGTCATTCCTGAAGTGAACAGATATGTAAGCTTACCTCCAGAGT 360
 QY 361 CTGAGCTATCTGCTGTTTGGAGAAACTTAAGAGTACAGCTATGAGAGCCCTTCTG 420
 Db 361 CTGAGCTATCTGCTGTTTGGAGAAACTTAAGAGTACAGCTATGAGAGCCCTTCTG 420
 QY 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAAAGCTACAGTCTCTT 480
 Db 421 CAAGAGGGAGAGCCTCTGGAACAGTGTACAGTGGGAGAGAAAGCTACAGTCTCTT 480
 QY 481 GTGAAGGCTTATGAGATTTGCAATGAGTAAACCCCTGCATCCAGATATCTCCAGAG 540
 Db 481 GTGAAGGCTTATGAGATTTGCAATGAGTAAACCCCTGCATCCAGATATCTCCAGAG 540
 QY 541 CTACGCAAGATAGAGGAGCAAAATGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
 Db 541 CTACGCAAGATAGAGGAGCAAAATGAGATAGCTTGTCCCTGTTCAATGGGGAGCA 600
 QY 601 GATTGCTGTGATGTGTGACTTCTGGGGAGCAAGAACATATCTATGCTGCAAAACA 660
 Db 601 GATTGCTGTGATGTGTGACTTCTGGGGAGCAAGAACATATCTATGCTGCAAAACA 660
 QY 661 TGTGGGATCTGGCCCTTGAAGAGGGATCAAACTCCAGAAATTTGGTCCCAAGT 720
 Db 661 TGTGGGATCTGGCCCTTGAAGAGGGATCAAACTCCAGAAATTTGGTCCCAAGT 720
 QY 721 GCCCATGCTGATTTAAACAAAGCAGCTTACTTTGGATGAGATTTGCGGGTCCCA 780
 Db 721 GCCCATGCTGATTTAAACAAAGCAGCTTACTTTGGATGAGATTTGCGGGTCCCA 780
 QY 781 TTGACGAAGATGATGAGAGTGTGAGGCAATGACAAAGCTATCTCCAGAAACT 840
 Db 781 TTGACGAAGATGATGAGAGTGTGAGGCAATGACAAAGCTATCTCCAGAAACT 840
 QY 841 GCCATGCTGCTGTTTACCCACAGTTTCTCATGTTGATATGATCTGCTCCCTGAA 900
 Db 841 GCCATGCTGCTGTTTACCCACAGTTTCTCATGTTGATATGATCTGCTCCCTGAA 900
 QY 901 GTGGCAAGCTGCTGTCAAAATACAAATACCCCTTCACTGTGAGCCTTGTCTGGAGGC 960
 Db 901 GTGGCAAGCTGCTGTCAAAATACAAATACCCCTTCACTGTGAGCCTTGTCTGGAGGC 960

Db 901 GTGGCCAGCTGGCTGTCAAAATACCCCTTCATGTGACACCTGTGTGGAGGC 960
 QY 961 TTCCTCATGCTCTTATGAGAAAGCAGATACCACTGGAGCACCATTGATTCGG 1020
 Db 961 TTCCTCATGCTCTTATGAGAAAGCAGATACCACTGGAGCACCATTGATTCGG 1020
 QY 1021 GTGAAAGGTGTAACCGCATTTGAGTGCACCCATTAAGTATGGCTATGCCCAAAAGC 1080
 Db 1021 GTGAAAGGTGTAACCGCATTTGAGTGCACCCATTAAGTATGGCTATGCCCAAAAGC 1080
 QY 1081 TCATCATGTGTGTATAGTGAACAAGATACAGAACTATGTTCTTCGTGATACA 1140
 Db 1060 ----- 1059
 QY 1141 GATTGGCAGGTGGATCTATGCTTCCCAACCATCGACGGCTGCGTGGCATT 1200
 Db 1060 ----- 1059
 QY 1201 AGCGCAGCTGTGGGCTGCTGATGACACTTGGTGAACGGCTATGTTGAAGCTACC 1260
 Db 1060 ----- 1059
 QY 1261 AAACAGATCATCAAAACTGCTGCTTCCTCAAGTACAGAACTGGAATATCAAGGCATC 1320
 Db 1060 ----- 1080
 QY 1321 TTTGTTTTGGGAATCCCAATTTGCTCATCTGCTGAGATCCCGTATTTTGACATC 1380
 Db 1081 TTTGTTTTGGGAATCCCAATTTGCTCATCTGCTGAGATCCCGTATTTTGACATC 1380
 QY 1381 TACCGCATCAAACTGATGACTGTAAGGGGTGAACCTTGACCAAGTTGCACTTCCCA 1440
 Db 1141 TACCGCATCAAACTGATGACTGTAAGGGGTGAACCTTGACCAAGTTGCACTTCCCA 1440
 QY 1441 CCCAGATTCATTTTGCATACATTAACACGCGGAGAGAGAGTACGATACAAATTC 1500
 Db 1201 CCCAGATTCATTTTGCATACATTAACACGCGGAGAGAGTACGATACAAATTC 1260
 QY 1501 CTAAAGGACATTCGAGAAATCTGTCACTCAATTCAGAAATCTTAAAGCGAAGCACCA 1560
 Db 1261 CTAAAGGACATTCGAGAAATCTGTCACTCAATTCAGAAATCTTAAAGCGAAGCACCA 1320
 QY 1561 GGAATGGTGGCATCATGCGCATGGCCAGACAACTGTTGACAGAAATGGTGGAGAA 1620
 Db 1321 GGAATGGTGGCATCATGCGCATGGCCAGACAACTGTTGACAGAAATGGTGGAGAA 1380
 QY 1621 TTTGCTCTCAGCTCTTCTGGACAGCTTGTACAGACGACGACGCTGACCCAGGAGCCAG 1680
 Db 1381 TTTGCTCTCAGCTCTTCTGGACAGCTTGTACAGACGACGACGCTGACCCAGGAGCCAG 1440
 QY 1681 ATGAATGTTCTTCACAAACCCCACTGA 1707
 Db 1441 ATGAATGTTCTTCACAAACCCCACTGA 1467
 RESULT 8
 ID ABL14565 standard; cDNA; 1746 BP.
 AC ABL14565;
 XX 26-MAR-2002 (first entry)
 DE Drosophila melanogaster expressed polynucleotide seq ID NO 38177.
 XX
 KM Drosophila: developmental biology; cell signalling; insecticide;
 XX pharmacological; gene; ss.
 OS Drosophila melanogaster.
 XX
 PN WO200171042-A2.
 XX
 PD 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.
 PF
 XX 23-MAR-2000; 2000US-191637P.
 PR 11-JUL-2000; 2000US-0614150.
 XX
 PA (PEKE) PE CORP NY.
 PI Venter JC, Adams M, Li PMD, Myers EW;
 DR WPI: 2001-65860/75.
 DR P-PsDB; ABB70462.
 XX
 PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -
 PS Claim 1; SEQ ID NO 38177; 21bp + Sequence Listing; English.
 CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB101840-AB116175), expressed DNA
 CC sequences (AB101840-AB116175) and the encoded proteins
 CC (AB101840-AB116175).
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcl_sequences.
 XX
 SQ Sequence 1746 BP; 393 A; 471 C; 484 G; 398 T; 0 other;
 Query Match 23.5%; Score 401.6; DB 23; Length 1746;
 Best Local Similarity 55.4%; Pred No. 2.8e-117;
 Matches 864; Conservative 0; Mismatches 684; Indels 12; Gaps 4;
 QY 110 ATGAGCCCTGGCAGCTAATTCATGATGATGCTGTGACCCCTGATAGTCTGGGAT 169
 Db 179 AGGAGCCCTGGCAGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 238
 QY 170 ATGATGTTCTTCCAGCCAGAGATTTATGCTCAAGTTTAAAGAAATGTTTAAAC 229
 Db 239 GGAGCTGTGATGCTGCGAGTGAATCTTAACTTGTGAGAGCCCTGCTTAAAT 298
 QY 230 TCACAGAGAGATGCGCATTAATGTCGTAAGTCAAGTGAACAGAGACCAAG 289
 Db 299 TTGGCAAGAGATTCAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
 QY 290 ATGATATTAGCAAGACATGCTATTCCTGAAGTGAACAGAGTATGGAAGCTTTAC 349
 Db 359 ACGACTTCGAGAGCAAGAAATCAAAAGAGCAAGCCCACTTACCTCTGGAAGCTGTC 418
 QY 350 CCTCCAGGCTGAGAGCTATCTGCTGTTTGGAGAACTTAAAGAGTAC---AGTCTA 406
 Db 419 CCGAGAGAGGACTCAGCAAGAGAGAGATCTCCGATGTTGATGATGATGATGATGAT 478
 QY 407 TGGAGCCTTCTGCAAGAGAGAGAGAGCTCTGGAACAGTGTACAGTGGGAGAGAAAC 466
 Db 479 GTACATACAACTGGCGCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
 QY 467 TCAGTGAAGCTCTTGTGAAGCTTATGAGATTTTGCATGAGATTAACCCCTGATCCAG 526
 Db 539 TGGTGGAGCTGCTCACTGAAGTATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 598
 QY 527 ATATCTTCCAGAGCTACCAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 586
 Db 599 ATCTTTTCCCGGAGTTTGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 658
 QY 587 TCAATGGGAG 646
 Db 659 TCATATGAGAACTACGACAGCTGTGGAACCATGACACCGGCGGACCAAGTACATTGTAA 718


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QY 647 TGGCTGCAAGCATGCGGATCTGGCCCTTTGANG---AAGGGATCAAAACTCCAGAAA 703
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 719 TGGCCATGAAGGCGGTACAGGATTTGCTAGAGATGCAAGGGATCACAGGCCAACA 778
QY 704 TTTGGCTCCCAAGTGGCCATGCTGATTTAACAAGCAGCCAGTACTTGGGATGA 763
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 779 TCGTGGTGGCTTAAGACGCTCAGCGGCTTCACAGGCGGTCACTTAAATATCC 838
QY 764 A---GATTTGGCGGCTCCATTCAGCAAGATGATGGATGTGGAGGCAATGAA 820
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 839 ACCTGGATCCGTGGATGATGATCCGAGACCTACGAGTGGACATTTAAGATTTCAAC 898
QY 821 GACCTATCTCCAGAAACACTGCTGCTGCTTGTACCCACAGTTCCTCATGCTG 880
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 899 GTGCCATTAACAGAAACAGATTCCTGCTGGTGGCTGCTCCGAATCTCCCATATGAA 958
QY 881 TAATAGATCTGTCCTGAAAGTGGCCAGCTGGCTGTCAATTAATAATACCCCTTATG 940
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 959 CCATCGATGACATGGAAGTATGCGCCCTTTGGCGCTTAAGTACGACATTCCTCGTCACG 1018
QY 941 TCGACGCTGTCTGGGAGCTTCCTCATGCTTATGGAAGCAAGATACCCACTGG 1000
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1019 TGGACGCTGCTGCGGAGCTTTGTGTGCTGCTGCTGCGCACGCGGCTATAGCT-- 1076
QY 1001 AGCACCCTTTGATTTCCGGGTGAAGGTAAACACAGCATTTGAGTACACCATAGT 1060
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1077 -GGTCCCTTCGACTTGAAGTCAAGGATGACGACTATCTCCGCTGATACCCACAAGT 1135
QY 1061 ATGGCTATGCCCCCAAAAGCTCATCATGTTGTTGATAGTACAGAGATACAGAACT 1120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1136 ATGCTTTCGCGCCCAAGGAGTATCGGTGATCTCTTACTCGAGCAAGATACAGAGACC 1195
QY 1121 ATGAGTCTCTGCGATGACAGATGAGAGTGGAGGCTGACATCTATGCTCCCAACCATTCAG 1180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1196 ATGAGTCTCTGAGTACTGACTGAGTGGCTGCGCGGTGATGTTGCTCCACAGTCAAGC 1255
QY 1181 GCTCAGCGCTGTGTCATTAAGCAGCAGCTGTTGGGCTGCTGATGACATTCGCTGAGA 1240
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1256 GTTCCGCTGGCGGAGTATATGCGCGCTGCTGGCTTACCATGATAGCTTTGGCTATG 1315
QY 1241 AGCGCTATGTTGAAGCTACCAAAACATCATCAAACTGCTCGCTTCTCAAGTCAAGAC 1300
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1316 ATGCTTATCTGAAGCAGCAGTACGAGTGTGATACGCGCGCTATATGAGAGGGGCGC 1375
QY 1301 TGGAAATATCAAGAGCATCTTTGTTGGGAATGCCCAATGCTCATGCTCTGG 1360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1376 TTGCGCGCATGATGGCATCTTATCTTGGCAAGCCAGCTACTTCAATGATTCCTGG 1435
QY 1361 GATCCCGTATTTTACATCTACGAGTATCAAACTGATGACTGCTAAGGGGTGAAGT 1420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1436 GTTCCATATGTTTGAATTTTCGGGCTATCGGATTCGATGCAAACTGGGCTGGAAC 1495
QY 1421 TGAACCATGTTGCACTTCCACCAAGTATTTATTTTGCATACATTAACACGCGCGGA 1480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1496 TGAATGGCTGCACTGTTCACTGATTCACCTGCTGACGAGCATGCACACAGC 1555
QY 1481 AAGAGATATATCAATCTCTAAAGCAATTCAGAGATGAGATGCTACATCAATATGAGA 1540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1556 CCGGAGTGGCGGATTAATTTATTTGCGATGTGGCAGCTGACGGCGGAGTCTATGAGG 1615
QY 1541 ATCTTAAGCAAGAGACCAAGATGGGTCCATTCATGCTGATGGCCAGACCAACTTTG 1600
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1616 ATCCGGGCAAGCCCGTGTGGAAAGATGCTCTAGGAGATGAGCAAGAGCATATACCG 1675
QY 1601 ACAGGAATATGTTGCAAAATTTGCTCACTTTCTTGGACAGCTTTACAGACGAGCA 1660
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1676 ACCGTTGCGTATGAGAGAGATGCTGCTATTCCTGCACTCATGATACACTCCA 1735

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RESULT 9
ABLI4555
ID ABLI4555 standard; cdna: 1782 BP.
XX

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AC ABLI4555;
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 38147.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001MO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW,
XX
XX WPI: 2001-656860/75.
XX
XX P-PsDB: ABB70452.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 38147; 21np + Sequence Listing: English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABLI16176-ABLI30511), expressed DNA
XX sequences (ABLI01840-ABLI16175) and the encoded proteins
XX (ABBI7737-ABBI2072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1782 BP; 410 A; 493 C; 486 G; 393 T; 0 other:
XX
XX Query Match 23.5%; Score 401.6; DB 23; Length 1782;
XX Best Local Similarity 55.4%; Pred. No. 2.8e-117;
XX Matches 864; Conservative 0; Mismatches 684; Indels 12; Gaps 4;
XX
QY 110 ATGAGCCCTGGCACTAATTCATGAGAGTGTGCTGAGACCTCTCTATAGTGGGAT 169
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 215 AGGAGCCCTGGCAGTGGCCACCATCAACGCGCACAGGCTGGAGGGCTGTGGCTCT 274
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 170 ATGAGTTGTCTTCCAGCCAGAGAGTGTATGCTCAAGCTTTAAAGAAATGTTTAAAGC 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 275 GGAATGATCTGCAAGATGAATTAATCTTTACATTCGTGGCAAGCTGATCTTTAAGT 334
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 230 TCACAGGAAGATGCCATTAATTTGCTGATAGATTCAAGCAAGCTTGAAGCAAGCAAG 289
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 335 TTGCGAAGAAAGATTCCAGCGGTGCTGCTGAGGTGGAGACTGAATTTGCCAAGCCAAA 394
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 290 ATGATATTACCAAGAAATGCTCATCTCTGAAAGTGGCAAAAGATATGTGAAAGCTTTAC 349
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 395 ACGACTTCGAGACGAATCAAAAAGAGACGCCCTTACCTACTCGAAACCTCTGC 454
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 350 CCTCCAGGCTGCTGATCATCTGCTGTTTGGAAACTTAAGAGATAC---AGCTCTA 406
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 455 CCGAAGAGGACTACGACAGAGAGATCTCTCGACTGTGTGATGATGACACTGTAAGACTG 514
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 407 TGAACGCTTCTGGCAAGAGGGAGAGACCTCTGTGAAACAGTGTACAGTGGGAGAGAGAAC 466
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

D	515	GTCACTCAACATGGCGTGTATGTCGTGTATCTGGCGGGTCTACGGCTACAAAGCTGATC	574
Q	467	TCACGTAGCTCCTTGTGTAAAGCCTTATGAGATTTTTCATGTGAGTAAACCCCTCGATCCAG	526
D	575	TGTGTGGAGCTGTGTACGTGAAGTGTAGCGCAAGGCCCTCTTACACCAATCCCTTTGGACGCG	634
Q	527	ATATCTTCCCAAGACTACGCAAGATTAAGGACAGAAATTTGAGGATAGCTGTTCCTGT	586
D	635	ATCTTTTCCCGGGAGTTTGGCAAAATGGAGCGGGAGGTAGTGGCATGGCATGCAACCTGT	694
Q	587	TCAATGGGGGACAGATTCTGTGTGATGTGACTTCTGGGGAAACAGAAAGCATPACTCA	646
D	695	TCCATGTGAAACTCAGCCAGCTGTGGAAACATAGACACCGGGCGGACCGAAATCCATTGTGAA	754
Q	647	TGGCGTCAAAAGCATGTGCGGATCTGGCCTTTGAG---AAGGGATCAAAATCCTAGAAA	703
D	755	TGGCATGAAAGGCTACAGGGATTTTCGTAGAGGTACAAAGGATACACAGGCCAACCA	814
Q	704	TTGTGCTCCCAAAAGTGCCCATGCTGCATTTTAACAAAGCCAGCTATTGTGGATGA	763
D	815	TCGGGTGGCCCTAAGACGGTCCACGCGGCTTGCACAAAGGGCGGTACAGTATTAAATACC	874
Q	764	A---GATTGTGGGGTCCCATTTGACAAAGATGATGGAGTGGATGTGAGGCATAGAGA	820
D	875	ACGTGCGATCCGTGTGATGTAGATCCGGAGACTACGAAAGTGGACATTTAAGAAATTCAAC	934
Q	821	GAGCTATCTCCAGAAACACTGCGATGCTGTCTTTTACCCCAAGTTTCTCATGTGTG	880
D	935	GTGCCATTAAACAGAACACGATCTGCTGGTGGGTGTCTCGAAGCTTCCCATATGGA	994
Q	881	TAATAGATCCGTCCCTGGAAGTGGCCCAAGCTGCGTGTCAATATCAAAATACCCCTTATG	940
D	995	CCATCGATGACATCGAAAGCTATCCGCCCTTTGGGCGTTAACTAGACATTTCCGTGCACG	1054
Q	941	TCGACGCTGTGCTGTGGAGGCTTCCATCGCTTTATGAGAAAGACAGATACCACATGG	1000
D	1055	TGAGACGCTGCGTGTGGCAGCTTTGTGGTGGCCTTGTCGCGAAGCCGCGCTATAAGCT--	1112
Q	1001	AGCACCATTTGATTTCCGGGTGAAGGTGTAAACGACATTTCACTGACACCCATTAAGT	1066
D	1113	-GCTCTCCCTTCGACTTTGAGGTCTCAAGGAGTGAACAGTATCTCCGCTGATACCCACAAGT	1171
Q	1061	ATGGCTATGCCCCAAAAGGCTCAATCTGTGTTGTATGAGCAAGAAAGTAAAGCAAGCT	1120
D	1172	ATGCTTTCGCGCCCAAGGGATCATCGTGGTATCTTTTACGTGGGAAGAAAGTACAAAGACC	1231
Q	1121	ATCAGTTCTTTCGTGATACAGATTGGCAGGGTGGCATCTATGCTTCCCAACCATTCGACG	1180
D	1232	ATCAGTTACAGTGTACTACTGACTGTGGCGTGGCGGGGTGTATGTTCCTCCACAGTCAACG	1291
Q	1181	GCTACGGCGCTGTGTGGCATTAAGCCAGCCTTGTGGGCTGGCTTGTATGACACTTTCGGTGA	1240
D	1292	GTTCCTCCGTGCGGAGGTATTATCCCGCGCTGCTGGGCTAACCATATGAGCTTTGGCTATGTG	1351
Q	1241	ACGGCTATGTTGGAAGTACCAAAACAGATCATCAAAACAGTCCGCTCCCTCAAGTCAGAAC	1300
D	1352	ATGCTTATCTGGAAGCCATTAAGGCATGTGTGATAGCGCGCGCTATATTCGAAGAGGGCG	1411
Q	1301	TGGAATAATATCAAAAGCATCTTTGTTTTGGGAATCCCAATTTGTCACTAATTCGCTGTG	1366
D	1412	TTTCGCGACATCGATGGCATCTTTTATCTTTTGGCAACCCAGCTACTCACTGATGTTCGCCCTGG	1471
Q	1361	GATCCCGGATTTTGAATCATACGAGCATATCAAACTGATAGCTGTAAAGGGTGGAACT	1420
D	1472	GTTCCAATGTGTGTGACATTTTCCGCGCTATCGGATTCGCTGTCAAACTGGGCTTGGAAAC	1531
Q	1421	TGAACAGTTGAGTGTCCCAACCCAGTATCTATTTCTGTGCATCATTTACTACACGCCCGGA	1480
D	1532	TGATGTGGCTGACATTTTCATCTGTATCCACTGTGGGTAGCAGACATGCACACAGC	1591
Q	1481	AACAGATGATATACAAATTCCTTAAAGACATTCGAGAAATCTGTACTATCAATCATGAMA	1540
D	1592	CCGGAATTCGCGATTAATTTATTTCCCAATGTGGCAGCTGTACGCGCGGAGTCTATGAAG	1651

OY		154L ATCTTAAGACGAGAACCAACAAGAATGGGTGCATATTTCGCGTCCGCCAGCACCCTGTG	1600
Dd		1652 ATCCCCGCCACGCCCGTGTTGGAAAGATGGCTCTCTTAGCGCATGGCACAGAGCATACC	1711
OY		160I ACAGGAATATAGTGTTGCAATAATTGTCCTCAGTCTTCTTGACACAGCTTGATACAGCACA	1660
Dd		171Z ACGCTTGCGTGATCGAAGAAAGTACTCGCCATATCTCGACACTCATGTACTACACTCCA	1771
RESULT 10			
AAD06842 ID			
AAD06842 standard; DNA:	2060 BP.		
AAD06842;			
XX			
DT	03-AUG-2001	(first entry)	
DE		Drosophila melanogaster sphingosine phosphate lyase (SPL) cDNA.	
KW	Fruit fly;	sphingosine phosphatase Lyase; SPL; metazoan; insect;	
XN	worm;	pesticidal agent; therapeutic; pesticide; drug target; ss.	
OS		Drosophila melanogaster.	
FT	Key CDS	Location/Qualifiers 110..1747 /tag-a	
PX		/product= "sphingosine phosphate lyase (SPL)"	
MW	MO200142479-A2.		
PD			
PN	14-JUN-2001.		
PF	07-DEC-2000;	2000KO-US33320.	
PR	08-DEC-1999;	99US-0169610.	
PT	28-DEC-1999;	99US-0173228.	
PI	28-DEC-1999;	99US-0173349.	
PA	(GENO-) GENOPTERA LLC.		
PI	Ebens AJ,	Keegan KP,	Stout TJ;
DR	WP1: 2001-381698/40.		
PS	P-PSDB: AAEO3543.		
Claim 3;	Page 57;	58pp; English.	
The invention relates to Drosophila melanogaster helicase protein, phosphatidylinositol transfer protein (PIP), sphingosine phosphate lyase (SPL) protein and their corresponding nucleic acid molecules. These nucleic acids and proteins are useful for genetically modifying the metazoan invertebrate organisms such as insects and worms, resulting in expression or mis-expression of the encoded proteins. The genetically modified organisms or cells are used in screening assays to identify candidate compounds which are potential pesticide agents or therapeutics that interact with subject proteins. The invention also relates to method for studying the biological activity of subject proteins and identifying compounds that have utility as pesticides. The nucleic acids are useful for generating mutant phenotypes in animal models or in living cells that is used for studying the regulation of proteins and use of proteins as pesticides and drug targets. The present cDNA sequence encodes <i>Drosophila melanogaster sphingosine phosphatase lyase (SPL) protein.</i>			
Sequence 2060 BP;	494 A;	541 C;	532 G; 493 T; 0 other;
Query Match	23.5%;	Score 401.6;	DB 22; Length 2060;
Best Local Similarity	55.4%;	Pred. No. 3.le-117;	


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Db      785 TTGTCCTCCGTAAGTGCATGCTGGTTGGACAAAGCTGCTATTACTTTGGCATGAGC 844
Qy      767 TTGTGGGGGTC---CCATTGACGAAGATGATGAGGTTGGAGGGCAATGAGAAG 823
Db      845 TAGGCCACGTGAGATGATGACAGACATATCAAGTGGACCTGGGAAAAGTGAATAAT 904
Qy      824 CTATCTCCAGACACTGCTGCTGTTCTTCTACCCAGTTTCCATGATGTAA 883
Db      905 TCATCAATAGAAACAAATTTTACTGTGCGGTCCGCTCCAACTTTCATGATGTTG 964
Qy      884 TAGATCTCTGCTGGAAGTGGCCAGCTGCTCAATATCAAAATACCCCTTCATGTCG 943
Db      965 CCGATGATATTGAAGGATTTGGTAAATATGACAAAATAATTAACCTTTCATGACGTCG 1024
Qy      944 ACCGTGCTCGGAGGCTTCTCATGCTCTTATGGAAGAACAGATACCCACTGAGC 1003
Db      1025 ACAGTTGCTGAGTTCTCTTATTTGTTTCAATTTATGAAAAGCTGGTTACAAAATCTGC 1084
Qy      1004 ACCCAATTTGATTTCCGGGTGAAGGTGTAACAGCATTTTCAGCTGACACCCATAGTATG 1063
Db      1085 CATTACTTGACTTGAAGTCCCGGAGTCACTCAATATGATGACACCTCATTAATATG 1144
Qy      1064 GCTATGCCCCAAAGGCTCATATGCTGTTGATAGTACAAAGATACAGAACTATC 1123
Db      1145 GATTTGACCAAAAAGCTCGTCAATATATATAGAAACAGGACTTACGAATGCATC 1204
Qy      1124 AGTTCTTCGTGATACAGATTTGGCAGGTTGGCATCTGCTCCCAACCATGCGAGCT 1183
Db      1205 AGATTACGTAAATCTCTGTTGACGTGGCGGTTATATGAGTCTCCATTAATGACAGGT 1264
Qy      1184 CACGCGCTGCTGCAATAGGCGAGCCGTGTTGGGCTGCTGATGCACTTGGTGAGACG 1243
Db      1265 CCAAGCGCTGGTGAATTTGTTGTTGTTGGGCACTATGTCATATGATGGTGAATATG 1324
Qy      1244 GCTATGTTGAAGTACCAAAAGATCATCAAACTGC---TCGCTCTCAAGTCAGAAC 1300
Db      1325 GGTACATATGAGTGTGCGCAAGAAATAGTCCGTGCGCAAGAAATGTTAAAAATACATCC 1384
Qy      1301 TGGAAATATCAAAAGCATTTGTTTGGGAATCCCAATGTCACATGCTGCTGG 1360
Db      1385 AGGAAACATTTCCAGACCTGAATATATGAGCAACCCCTAGATATTCAGTCAATTTTCAATTTT 1444
Qy      1361 GATCCGCTGATTTTGCATCTACCGACTATCAAACTGATGACTGTAGGGGTGGAAC 1420
Db      1445 CTTCAAAGACCTTGAACATACAGAACTATCTGACAGTTGTCCAAAGAAAGGTGGCAT 1504
Qy      1421 TGAACCAAGTTCGACTCCACCCAGTATTCATTTCTGATCACAATTCACGCC 1477
Db      1505 TCAATGCCCTACAAAAGCCGTTGCACTACACATGAGCTTCACGAGATTGAGCGCTC 1561

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RESULT 13
AAH29742
ID AAH29742 standard; DNA; 2270 BP.

AAH29742:
XX
XX 27-JUL-2001 (first entry)
XX
XX S cerevisiae apoptosis associated coding sequence YDR294C.
XX
XX Yeast; fungus; apoptosis; infection; proliferative disease;
XX
XX vaccine; autoimmune disease; ischemia; neurodegeneration; ds.
OS
XX Saccharomyces cerevisiae.
XX
XX MO200102550-A2.
XX
XX 11-JAN-2001.
XX
XX 03-JUL-2000; 2000WO-BE00077.
XX
XX 01-JUL-1999; 99EP-0870141.
PR

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XX  
PA (JANC) JANSSEN PHARM NV.  
XX  
XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL.  
PI Nelissen BJM, Reekmans RJ.  
XX  
XX WPI: 2001-367042/38.  
DR P-PSDB: AAG70706.  
XX  
XX  
XX Yeast and fungal nucleic acids encoding proteins involved in a pathway  
PT leading to programmed cell death, useful for treating proliferative  
PT disorders, yeast and fungal infections, or for preventing apoptosis in  
PT certain diseases -  
XX  
XX  
XX Claim 1: Fig 1: 218pp: English.  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of apoptosis associated proteins from the yeast Saccharomyces  
CC cerevisiae and the fungus Candida albicans. These can be used to identify  
CC treatments for fungal and yeast infections, for proliferative diseases  
CC and for apoptosis related diseases such as autoimmune diseases, ischemia  
CC and neurodegeneration. The present sequence is one of the S. cerevisiae  
CC coding sequences of the invention.  
XX  
SQ Sequence 2270 BP; 707 A; 450 C; 467 G; 646 T; 0 other:  
  
Query Match 15.0%; Score 256.2; DB 22; Length 2270;  
Best Local Similarity 55.0%; Pred. No. 1.2e-70;  
Matches 592; Conservative 0; Mismatches 473; Indels 12; Gaps 4;  
  
Qy 413 CCTTCTGCAAGAGGAGGAGACCTCTGACAGTGTACAGTGGGAGAGAACTCAGT 472  
Db 985 CCAATGGAAGGAAGGAAGGTCTGCTGCGCTTACCAAGGTGATGATTTGATCC 1044  
Qy 473 AGCTCTTGTGAAGCTTATGAGATTTGATGAGACTAACCCCTGCATCAGATATCT 532  
Db 1045 ACTTACAAACATCGCATACGAAATAATTTGCGTTCATTAATTCATCCCATCT 1104  
Qy 533 TCCAGAGTACGCAATATGAGGAGCAAAATTTGAGAGTATGTTCCCTGTTCAAT 592  
Db 1105 TTCTGCGGTACGTAATATGAAATCCGAAAGTGTCTTATGTTTAAAGATGTTTATG 1164  
Qy 593 GGGGACGAGATTCGTGTGATGTGTG---ACTTCTGGGGGAACGAAGCATCTCATGG 649  
Db 1165 CCCCTTGATACAGGTTGTGTTGATACCAACTTCAAGTGTGATGAGAAATCTGTTTATG 1224  
Qy 650 CTGCAAGCATGTGCGGATCTGCGCTTTGAGAA---GGGATCAAAATCTCAGAAATTG 706  
Db 1225 CATGCTGAGCGCTAAATATGATGCTCTTATCATCTGTGAAATCAGCAACCAAAATTA 1284  
Qy 707 TGGCTCCCAAGAGGCCATGCTGATTTAAACAAAGCAGCTTACTTTGGATGANA 766  
Db 1285 TTGCTCCGTTACTGCAATGCTGGGTTTGACAAAGCTGCTTATTTAGCTTGGCATAGC 1344  
Qy 767 TTGTGCGGGTC---CCATTGACGAAGATGATGAGTGTGATGAGGCAATGAGAAG 823  
Db 1345 TAGCCACGTGAGACTGTATGATCAACGATATCAAGTGAAGCTGGAAAGTGAATAAT 1404  
Qy 824 CTATCTCAGGACACAGCTGCTGCTGTTTACCCACAGTTTCTCATGATGTAA 883  
Db 1405 TCATCAATTAAGAACATATTTACTGTGCGTTCCGCTCCAAATCTTCATATGTTG 1464  
Qy 884 TAGATCTGTCCTGGAAGTGGCCAAAGCTGCTCAATATCAAAATACCCCTTCATGTCG 943  
Db 1465 CCGATGATTTGAAGAGTTGGGTAAATAGCACAAAATATTAACCTTCTTTACACGTCG 1524  
Qy 944 ACCTTGTCTGGAGGCTTCTCATGCTTTATGAGAAAGCAGATACCCACTGAGC 1003  
Db 1525 ACAGTTGCTAAGGTTCTTATTTATGTTTATGGAAGAGGCTGTGTAATAATCTGC 1584  
Qy 1004 ACCCAATTTGATTTCCGGGTGAAGGTATACACGATTTTCACTGACACCATATGATG 1063  
Db 1585 CATTACTTGACTTGAAGTCCCGGAGCTCACTCAATATCATGATGACACTCATTAATATG 1644

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QY 1064 GCTATGCCCAAGGCTCATCTGTTGTATAGTACAGAAAGTACAGAACTATC 1123
 DB 1645 GATTTCACCAAAAGGCTGCTGATATATATAGAAAGAGCGCTTACGAATGCATC 1704
 QY 1124 ACTTCTGTCATACATTTGGCAGGGGCGATCTATGCTTCCCAACATCGAGCT 1183
 DB 1705 AGTATTTAGCTAATCTGCTTGGACTGGCGGTTATATGCTCTCTACATTAGCAGGCT 1764
 QY 1184 CAGGCGCTGTCGATTAAGCCGAGCGCTGTTGGCTGCTTGAATGCACTTGGTGAGACG 1243
 DB 1765 CAGGCGCTGTCGATTAAGCCGAGCGCTGTTGGCTGCTTGAATGCACTTGGTGAGACG 1824
 QY 1244 GCTATTTGAGCTACCAAAAGCATATCAAAAGTGC---TTCGCTTCTCAAGTCAAGAC 1300
 DB 1825 GGTACATTTAGCTGCTGCGCAAAATATGTCGTCGACAGCATGAATTTAAATAATACATCC 1884
 QY 1301 TGGAAATATCAAAAGCATCTTGTGTTTGGAAATCCCAATGTCACATCTGCTGCTG 1360
 DB 1885 AGGAAACATTTCCAGACCTGAAATATATATGCGAACCCCTAGATATTCATGCTATTTATTT 1944
 QY 1361 GATCCCGTGTATTTGACATCTACGACTATCAAACTGATGACTGCTAAGGGGTGAAC 1420
 DB 1945 CTTCAAAAGCTTGAACATACGACATATCTGACAGGTTGCCAAGAAAGGCTGCAAT 2004
 QY 1421 TGACCAAGTTGCAATTCCTCCACCCAGTATTCATTTGCAATCACTTACTACAGGCC 1477
 DB 2005 TCAATGCCCTACAAAGAGCGGCTTGCACTACACATGAGCTTACAGATTTAGCGCTC 2061

RESULT 14

AAK25568
 ID AAK25568 standard; cDNA; 1629 BP.

AC AAK25568;

DT 02-AUG-1999 (first entry)

DE C. elegans sphingosine-1-phosphate lyase cDNA.

XX Sphingosine-1-phosphate lyase; SPL; breast cancer; diagnosis;

KW prognosis; therapy; ss.

XX Caenorhabditis elegans.

XX WO9116888-A2.

XX 08-APR-1999.

XX 29-SEP-1998; 98WO-US20365.

XX 29-SEP-1997; 97US-0939309.

XX (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.

XX Saba JD, Zhou J;

XX WPI; 1999-263700/22.

XX P-PsDB; AAY05828.

XX Sphingosine-1-phosphate lyase, polynucleotides and modulators

XX Example 2; Page 75-79; 96pp; English.

XX This is the nucleotide sequence of Caenorhabditis elegans cDNA
 CC coding for sphingosine-1-phosphate lyase (SPL, see AAY05828). The
 CC SPL cDNA was obtained by systematic sequencing of the C. elegans
 CC genome. SPL catalyses the cleavage of sphingosine-1-phosphate into
 CC inactive metabolites. Human sphingosine-1-phosphate is an
 CC endogenous tumour suppressor lipid that potentially inhibits breast
 CC cancer cell growth and invasiveness, while not affecting the growth
 CC of non-tumour cells. Mouse and human SPL polynucleotides (see
 CC AAK25666-67) and polypeptides (see AAY05826-29) are claimed. Methods

CC for preparing SPL polypeptides using transformed or transfected
 CC host cells are provided. Human, mouse, C. elegans or yeast SPL
 CC polypeptides can be used in claimed methods for identifying agents
 CC that modulate SPL activity. SPL inhibitors will inhibit growth of
 CC cancer cells, especially breast cancer cells. SPL inhibitors,
 CC including polynucleotides preventing expression of SPL genes, or
 CC antibodies against SPL, can also be used to prevent the development
 CC and/or metastasis of cancer, especially where the inhibitor is
 CC linked to an antitumour or antileukemia receptor antibody.
 CC Detection of alterations in an endogenous SPL sequence can be used
 CC to diagnose cancer, and to assess the prognosis for recovery.

XX Sequence 1629 BP; 473 A; 322 C; 372 G; 462 T; 0 other;

Query Match 13.2%; Score 225.6; DB 20; Length 1629;

Best Local Similarity 53.0%; Pred. No. 6.1e-61;

Matches 589; Conservative 0; Mismatches 499; Indels 24; Gaps 4;

QY 424 GAGGGAGACCTCTGGAACAGTGTACAGTGGGAGG-----ACAGCTCAGTACCTC 477
 DB 382 GAAGGAGAGGTATCTGAGCAGCTTCAATAGAGAAGACGACAGGAGAGAGATG 441
 QY 478 CTTGGAAGGCTTATGAGATTGTCATGAGTAACCCCTGCATCCAGATATCTTCCA 537
 DB 442 TATGAGAGAGGTGTCGAAATATTCCTGACCAACCCACTTGGCCAAATTTGTTCCCT 501
 QY 538 GACATACGCAAGATAGAGGACGAAATTTGAGATAGCTTGTCCCTGTCATAGGGGGA 597
 DB 502 GGAGTGAAGATCATGAGAGGCTGAACTTGTCCCATGTGTTATATATGATGAGAT 561
 QY 598 CCAGATTGCTGTGATGTGACCTTCTGGGGGACAGAAAGCATCTAGGCTTGCAAA 657
 DB 562 TCGGAGACATGTGGAACATATGCAACCTGTCGATCATTTCAATCTTTGGCGCTG 621
 QY 658 GCATGTGGGATCTGCGCTTGTGAGAAGGGATCAAAACCTGCGAATTTGTGGCTCCCAA 717
 DB 622 GCTCATCTGTAATCTGCTTTTGAAGAGAGGAAAGTACACAGATATTTGCCATCA 681
 QY 718 AGTGCCATGCTGCAATTAACAAAGCAGCACTTCTTGGAGTGAAGATTTGGCGGCTC 777
 DB 682 TCCGTCATGACAGGCTTCTTCAAAAGCTGCGAATGTTCCGATCAAAAGTTCCGAAT 741
 QY 778 CCATT---GAGCAAGATGATGAGGTGATGTGAGGCAAGATGAGAGCTATCTCCAG 834
 DB 742 CCAGTTGATCTCTTACTTCAAAAGTACACCTTGTCAAAATGAAACCGCAATTAACAG 801
 QY 835 AACCTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 894
 DB 802 AGACATGATATGTTAGTTGATGATGATGATGATGATGATGATGATGATGATGAT 861
 QY 895 CCTGAAGTGGCCAAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 954
 DB 862 GAACTATTTGACAGCTAGGAGCTTGAATATGATGATGATGATGATGATGATGATG 921
 QY 955 GGAGCTTCTGATGCTGCTTATATGAGAAAGCAGATACCCACTGAGACACCATTTGAT 1014
 DB 922 GGTGCTTCTCTTCCATCTCTTGAAGAAAGC-----GAAATTCGCTATATAC 969
 QY 1015 TTCCGGTGAAGAGGTATACACGATTTACAGCTGACACCAATTAAGTATGGCTATCCCA 1074
 DB 970 TTCCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1029
 QY 1075 AAAGGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1134
 DB 1030 AAAGGCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1089
 QY 1135 GATACAGATTGGCAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1194
 DB 1090 GATGCTGATTTGGCAAGGAGGTATATCATCTGCTGCTGCTGCTGCTGCTGCTGCTG 1149
 QY 1195 GGCATTTACGAGAGCTGTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1254
 DB 1150 CACAACATTTGCACTTGTGCTGGGCGCAATGCTTTATACAGGCTCAGGAAGATACAGGCG 1209

QY	1255	GCTACCAAAACGATCATCAAAACGTCGCTTCCTCGAAGTGAAGACTGGAAAATATACAA	1314
Db	1210	AATCGTAAAGAAATGTTGGACACTCAAGAAAGATTTACAAATGGCACTTTCAAACTTTAAAG	1265
QY	1315	GGCATCTCTTTGTTGGGAATCCCAATGTGCACATCTGCTCGTGCGATCCCGTGAT---	1371
Db	1270	GGAATCAAAATTTACAAGGGCCAAGTATGTTGTATGTTGTTACTGCGACAAACCAATGATGGA	1329
QY	1372	TTTGACATCTACCGACTTCAAACTGATGACTGCTTAAGGGGTGSACTTGAAACCAGTTG	1431
Db	1330	GTTGAACCTCTACAGTTGTTCCATTACTTCATGGAAGAAAAACAATTTGGCACTAAATGGACTT	1389
QY	1432	CAGTTCGCCACCAAGTATCATTTCTGCACTACATTAACACGCCCGGAAAGCAAGTACT	1491
Db	1390	CAATTCCTCCAGCTGGAGTTCATATCATGTGTACTATGATTCATTAATCACTCTGGACTGCT	1449
QY	1492	ATACAAATTCCTAAAGACATCGAGAATCTGT	1523
Db	1450	GAAGCTTTGTCGCGCGATTTGGACAGCTGCAAT	1481

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Db      3323  GTCAAGGTTCCCGTCCGAGAGTATTATCGCGCTGCTGGCTACCATGATGAGCTTT 3382
Qy      1234  GGTGAGAACGGCTATGTGAAGCTACCAACAGATCATCAAAACTGCTGCTTCCCTCAAG 1293
Db      3383  GGCTATGATGTTATCTGGAAGCCACTAAGCCCATTTGTGATACGGCGGCTATATCGAG 3442
Qy      1294  TCAGAACTGGAATAATATCAAG 1315
Db      3443  AGGGGGTAAGTTTGTATCAAG 3464
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Job time : 487 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:50:19 : Search time 40 Seconds
(Without alignments)
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Title: US-10-053-510-8

Perfect score: 2977
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Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	12 US-10-197-073-4	Sequence 4, App11
2	2977	100.0	568	12 US-10-053-510-8	Sequence 8, App11
3	2977	100.0	568	12 US-10-286-175-4	Sequence 4, App11
4	2959	99.4	568	10 US-09-740-369-2	Sequence 2, App11
5	2959	99.4	568	12 US-10-053-510-18	Sequence 18, App11
6	2553	85.8	568	12 US-10-197-073-2	Sequence 2, App11
7	2553	85.8	568	12 US-10-053-510-6	Sequence 6, App11
8	2553	85.8	568	12 US-10-286-175-2	Sequence 2, App11
9	2498	83.9	488	12 US-10-197-073-10	Sequence 10, App11
10	2498	83.9	488	12 US-10-053-510-10	Sequence 10, App11
11	2498	83.9	488	15 US-10-286-175-10	Sequence 16, App11
12	1344	45.1	545	12 US-10-053-510-16	Sequence 11, App11
13	1082	36.3	552	12 US-10-053-510-11	Sequence 6, App11
14	1008	33.9	542	12 US-10-197-073-6	Sequence 4, App11
15	1008	33.9	542	12 US-10-053-510-4	Sequence 4, App11

16	1008	33.9	542	15 US-10-286-175-6	Sequence 6, App11
17	1007.5	33.8	589	12 US-10-197-073-8	Sequence 8, App11
18	1007.5	33.8	589	12 US-10-053-510-2	Sequence 2, App11
19	1007.5	33.8	589	15 US-10-286-175-8	Sequence 8, App11
20	355	11.9	76	10 US-09-740-369-4	Sequence 4, App11
21	244.5	8.2	509	12 US-10-167-547C-4	Sequence 4, App11
22	244.5	8.2	529	12 US-10-167-547C-6	Sequence 6, App11
23	233.5	7.8	496	15 US-10-006-852-12	Sequence 12, App11
24	233	7.8	500	15 US-10-006-852-16	Sequence 16, App11
25	228.5	7.7	496	15 US-10-006-852-14	Sequence 14, App11
26	227.5	7.6	496	15 US-10-005-602-2	Sequence 2, App11
27	227	7.6	454	15 US-10-156-761-11138	Sequence 11138, A
28	227	7.6	502	15 US-10-006-852-2	Sequence 2, App11
29	226	7.6	494	15 US-10-006-852-4	Sequence 4, App11
30	219.5	7.4	498	12 US-10-167-547C-2	Sequence 2, App11
31	216.5	7.3	470	15 US-10-156-761-12189	Sequence 12189, A
32	211.5	7.1	494	15 US-10-006-852-10	Sequence 10, App11
33	209	7.0	502	15 US-10-006-852-18	Sequence 18, App11
34	202	6.8	500	15 US-10-006-852-6	Sequence 6, App11
35	198	6.7	493	15 US-10-006-852-8	Sequence 8, App11
36	174.5	5.9	505	15 US-10-156-761-12806	Sequence 12806, A
37	167	5.6	480	15 US-10-156-761-13740	Sequence 13740, A
38	155.5	5.2	488	12 US-10-032-585-7216	Sequence 7216, App
39	150.5	5.1	393	10 US-09-712-363-264	Sequence 264, App
40	145	4.9	241	10 US-09-712-363-264	Sequence 11, App1
41	144.5	4.9	389	9 US-10-156-761-10293	Sequence 10293, A
42	144	4.8	393	9 US-09-846-590B-14	Sequence 14, App1
43	139	4.7	453	12 US-10-342-224-118	Sequence 118, App
44	131	4.4	457	15 US-10-156-761-13584	Sequence 13584, A
45	131	4.4	585	15 US-10-038-686-2	Sequence 2, App11

ALIGNMENTS

RESULT 1
US-10-197-073-4
Sequence 4, Application US/10197073
Publication No. US20030166897A1
GENERAL INFORMATION:
APPLICANT: Sabo, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Dravet, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116, 402D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid

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; MOLECULE TYPE: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-197-073-4
Query Match      100.0%: Score 2977; DB 12; Length 568;
Best Local Similarity 100.0%: Pred. No. 2.9e-287;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIVGYEYV 60
DB 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIVGYEYV 60
OY 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKDKDISKMMSFLKYDKKEYKALP50G 120
DB 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKDKDISKMMSFLKYDKKEYKALP50G 120
OY 121 LSSSAVLEKLEKESMDAFWQEGRASGVYSGEELTELIVKAYGDFAMSNPLHDPDIPG 180
DB 121 LSSSAVLEKLEKESMDAFWQEGRASGVYSGEELTELIVKAYGDFAMSNPLHDPDIPG 180
OY 181 LKRIAEIYRIACSLFNGPDSGCVTSQGTESIIMACKACRDIAFEKGIKTPETIAPOS 240
DB 181 LKRIAEIYRIACSLFNGPDSGCVTSQGTESIIMACKACRDIAFEKGIKTPETIAPOS 240
OY 241 AHAAPNKAASYGKMIYRVPLTKMMEVDVRAIRRAISRNTAMLCVSTPOFPHGVIDPVPE 300
DB 241 AHAAPNKAASYGKMIYRVPLTKMMEVDVRAIRRAISRNTAMLCVSTPOFPHGVIDPVPE 300
OY 301 VAKLAVKKYIPLHVACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGTAAPG 360
DB 301 VAKLAVKKYIPLHVACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGTAAPG 360
OY 361 SSLVLYSDKKYRNQYFVVDWQGIYASPTIAGSRPGISAAACMAALMHFEGENCYEAT 420
DB 361 SSLVLYSDKKYRNQYFVVDWQGIYASPTIAGSRPGISAAACMAALMHFEGENCYEAT 420
OY 421 KOITATAPLKSELENIKIGIFVFGNPQSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOITATAPLKSELENIKIGIFVFGNPQSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
OY 481 PSIHFCITLLHARKKRAVIOFLKDIRESVYQIMKNPKAKTTGCAIYAMAQTTVDNRMAE 540
DB 481 PSIHFCITLLHARKKRAVIOFLKDIRESVYQIMKNPKAKTTGCAIYAMAQTTVDNRMAE 540
OY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 2
US-10-053-510-8
; Sequence 8, Application US//10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-053-510-8
Query Match      100.0%: Score 2977; DB 12; Length 568;
Best Local Similarity 100.0%: Pred. No. 2.9e-287;
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Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIVGYEYV 60
DB 1 MPSTDLMLKAEPEYLEILEVYSTAKNVNCHCTKYEPMOLIAMSVWTLIIVGYEYV 60
OY 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKDKDISKMMSFLKYDKKEYKALP50G 120
DB 61 FOPESLMSRFKKCKRKLTKRMPIIGRKIODKLNTKDKDISKMMSFLKYDKKEYKALP50G 120
OY 121 LSSSAVLEKLEKESMDAFWQEGRASGVYSGEELTELIVKAYGDFAMSNPLHDPDIPG 180
DB 121 LSSSAVLEKLEKESMDAFWQEGRASGVYSGEELTELIVKAYGDFAMSNPLHDPDIPG 180
OY 181 LKRIAEIYRIACSLFNGPDSGCVTSQGTESIIMACKACRDIAFEKGIKTPETIAPOS 240
DB 181 LKRIAEIYRIACSLFNGPDSGCVTSQGTESIIMACKACRDIAFEKGIKTPETIAPOS 240
OY 241 AHAAPNKAASYGKMIYRVPLTKMMEVDVRAIRRAISRNTAMLCVSTPOFPHGVIDPVPE 300
DB 241 AHAAPNKAASYGKMIYRVPLTKMMEVDVRAIRRAISRNTAMLCVSTPOFPHGVIDPVPE 300
OY 301 VAKLAVKKYIPLHVACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGTAAPG 360
DB 301 VAKLAVKKYIPLHVACLAGFLIVFMEKAGYLEHPDFRVKGVTSISADTHKYGTAAPG 360
OY 361 SSLVLYSDKKYRNQYFVVDWQGIYASPTIAGSRPGISAAACMAALMHFEGENCYEAT 420
DB 361 SSLVLYSDKKYRNQYFVVDWQGIYASPTIAGSRPGISAAACMAALMHFEGENCYEAT 420
OY 421 KOITATAPLKSELENIKIGIFVFGNPQSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOITATAPLKSELENIKIGIFVFGNPQSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
OY 481 PSIHFCITLLHARKKRAVIOFLKDIRESVYQIMKNPKAKTTGCAIYAMAQTTVDNRMAE 540
DB 481 PSIHFCITLLHARKKRAVIOFLKDIRESVYQIMKNPKAKTTGCAIYAMAQTTVDNRMAE 540
OY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
DB 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 3
US-10-286-175-4
; Sequence 4, Application US//10286175
; Publication No. US20030059922A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed Intellectual Property Law Group
; STREET: 701 Fifth Avenue, Suite 6300
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98055
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/10/286,175
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Steven J.
; REGISTRATION NUMBER: 43,058
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; REFERENCE/DOCKET NUMBER: 200116.402C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-286-175-4
Query Match          100.0%; Score 2977; DB 15; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,96-287;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MPSTDLMKAFEPYLEILEVYSTKAKNVNGHCTKYPEPMOLIAHSVVTLLIYWGYEFV 60
DB 1 MPSTDLMKAFEPYLEILEVYSTKAKNVNGHCTKYPEPMOLIAHSVVTLLIYWGYEFV 60
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DB 61 FQPSLMSRFKKCKEKLTRKMPITGRKTODKLNTKDDISKMSFLKVDKEYVALPSQG 120
OY 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
DB 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
OY 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
DB 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
OY 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
DB 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
OY 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
DB 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
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DB 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
OY 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
DB 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
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DB 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
OY 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
DB 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
OY 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
OY 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
OY 481 PSIHFCITLHARRKRAVLAQFLKDIRESVTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
DB 481 PSIHFCITLHARRKRAVLAQFLKDIRESVTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
OY 541 LSSVFLDSLSTDTVTGSGQNGSPKPH 568
DB 541 LSSVFLDSLSTDTVTGSGQNGSPKPH 568
RESULT 4
US-09-740-369-2
; Sequence 2, Application US/09740369
; Patent No. US20020168710A1
; GENERAL INFORMATION:
; APPLICANT: DUCKWORTH, DAVID MALCOLM
; APPLICANT: GODDEN, ROBERT JAMES
; APPLICANT: TESTA, TANIA TAMSON
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30034-D1
; CURRENT APPLICATION NUMBER: US/09/740,369
; PRIOR APPLICATION NUMBER: EP 98300625.5
; PRIOR FILING DATE: 1998-01-29
; PRIOR APPLICATION NUMBER: UK 9824026.0
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; PRIOR FILING DATE: 1998-11-03
; PRIOR APPLICATION NUMBER: 09/238,373
; PRIOR FILING DATE: 1999-01-27
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 568
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-740-369-2
Query Match          99.4%; Score 2959; DB 10; Length 568;
Best Local Similarity 99.5%; Pred. No. 1,8e-285;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
OY 1 MPSTDLMKAFEPYLEILEVYSTKAKNVNGHCTKYPEPMOLIAHSVVTLLIYWGYEFV 60
DB 1 MPSTDLMKAFEPYLEILEVYSTKAKNVNGHCTKYPEPMOLIAHSVVTLLIYWGYEFV 60
OY 61 FQPSLMSRFKKCKEKLTRKMPITGRKTODKLNTKDDISKMSFLKVDKEYVALPSQG 120
DB 61 FQPSLMSRFKKCKEKLTRKMPITGRKTODKLNTKDDISKMSFLKVDKEYVALPSQG 120
OY 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
DB 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
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DB 121 LSSAVLEKLEKSSMDAFMOEGRASGVYSGEEKLTBLVKA YGDFAMSNPLHPDIPG 180
OY 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
DB 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
OY 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
DB 181 LKRTAEIVRIACSLFNGPDSGCVTSGGTESIIMACKACRDLAFEKGITPEIVAPQS 240
OY 241 AHAENKASVFGMKIVVPLTKMVEVDVRAARRAISNTAMLCSTQFPHGVTDVPE 300
DB 241 AHAENKASVFGMKIVVPLTKMVEVDVRAARRAISNTAMLCSTQFPHGVTDVPE 300
OY 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
DB 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
OY 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
DB 301 VAKLAVKKYKIPLHVDAICGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKKYAPBG 360
OY 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
DB 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
OY 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
DB 361 SSVLYISDKKRRNQFVFDTDWOGGIYASPTIAGSRPGISAAACAAALMHGEGNCYVAT 420
OY 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
OY 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
DB 421 KOITTAFLKSELENIGIFVFGNPQSLIALGSRDDIYRLSLMTAKGNLNQLOFP 480
OY 481 PSIHFCITLHARRKRAVLAQFLKDIRESVTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
DB 481 PSIHFCITLHARRKRAVLAQFLKDIRESVTOIMKNPKAKTTGMAIYMAAQTTVDNNVAE 540
OY 541 LSSVFLDSLSTDTVTGSGQNGSPKPH 568
DB 541 LSSVFLDSLSTDTVTGSGQNGSPKPH 568
RESULT 5
US-10-053-510-18
; Sequence 18, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyset, Henrik
; TITLE OF INVENTION: SPRINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 568
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TYPE: PR1
ORGANISM: Homo sapiens
US-10-053-510-18

Query Match
Best Local Similarity 99.4%; Score 2959; DB 12; Length 568;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYKPEWOLIAWSVWTLIWMGEFV 60
DB 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYKPEWOLIAWSVWTLIWMGEFV 60
QY 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTODISKNSFLKVKVEYKALPSOG 120
DB 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTODISKNSFLKVKVEYKALPSOG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEEKITELLYKAYGDFANSLPHDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEEKITELLYKAYGDFANSLPHDIFPG 180
QY 181 LKRIEAIYRIACSLFNGSPDSCGCVTSGTESILMACAKAYRDLAFKIKTPEIYAPQS 240
DB 181 LKRIEAIYRIACSLFNGSPDSCGCVTSGTESILMACAKAYRDLAFKIKTPEIYAPQS 240
QY 241 AHAFAFKASVYEGMKIVRPVLTFRKMEVDVYRAMRRAISRNTAMLYCSTPQFPHGVIDPVE 300
DB 241 AHAFAFKASVYEGMKIVRPVLTFRKMEVDVYRAMRRAISRNTAMLYCSTPQFPHGVIDPVE 300
QY 301 VAKLAVKXKIPLVHDAACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKXKIPLVHDAACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVLVYSDKKRYNYOFFVDTDWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
DB 361 SSVLVYSDKKRYNYOFFVDTDWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
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QY 481 PSIHFCITLLHAKRVAIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVVDRNVAE 540
DB 481 PSIHFCITLLHAKRVAIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVVDRNVAE 540
QY 541 LSSVFLDSLSTDTVTYQSGOMNGSPKP 568
DB 541 LSSVFLDSLSTDTVTYQSGOMNGSPKP 568

RESULT 6
US-10-197-073-2
Sequence 2, Application US/10197073
Publication No. US20030166897A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/197, 073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvalter, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116.40202
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-197-073-2

Query Match
Best Local Similarity 85.8%; Score 2553; DB 12; Length 568;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYKPEWOLIAWSVWTLIWMGEFV 60
DB 1 MSTDLMLKAFPEYLEIEVYSTKAKNYNGHCTYKPEWOLIAWSVWTLIWMGEFV 60
QY 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTODISKNSFLKVKVEYKALPSOG 120
DB 61 FQESLMSRKKKCFKLTFRKMPITGRKIDKLTODISKNSFLKVKVEYKALPSOG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEEKITELLYKAYGDFANSLPHDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEEKITELLYKAYGDFANSLPHDIFPG 180
QY 181 LKRIEAIYRIACSLFNGSPDSCGCVTSGTESILMACAKAYRDLAFKIKTPEIYAPQS 240
DB 181 LKRIEAIYRIACSLFNGSPDSCGCVTSGTESILMACAKAYRDLAFKIKTPEIYAPQS 240
QY 241 AHAFAFKASVYEGMKIVRPVLTFRKMEVDVYRAMRRAISRNTAMLYCSTPQFPHGVIDPVE 300
DB 241 AHAFAFKASVYEGMKIVRPVLTFRKMEVDVYRAMRRAISRNTAMLYCSTPQFPHGVIDPVE 300
QY 301 VAKLAVKXKIPLVHDAACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKXKIPLVHDAACLGFLIVEMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVLVYSDKKRYNYOFFVDTDWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
DB 361 SSVLVYSDKKRYNYOFFVDTDWOGGIYASPTIAGSRPGISAAQWALMHFGNGYVEAT 420
QY 421 KQIKTARFLKSELENIKIFVFGNPOSLIALGSDPDIYRLSNLMTAKGNLNOLOPP 480
DB 421 KQIKTARFLKSELENIKIFVFGNPOSLIALGSDPDIYRLSNLMTAKGNLNOLOPP 480
QY 481 PSIHFCITLLHAKRVAIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVVDRNVAE 540
DB 481 PSIHFCITLLHAKRVAIOFLKDIRESVQIMKNPRAKTGTGGAITYAMAQTVVDRNVAE 540
QY 541 LSSVFLDSLSTDTVTYQSGOMNGSPKP 567
DB 541 LSSVFLDSLSTDTVTYQSGOMNGSPKP 567

RESULT 7
US-10-053-510-6
Sequence 6, Application US/10053510
Publication No. US20030173939A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
APPLICANT: Fyrist, Henrik
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
POLYNUCLEOTIDES AND MODULATING AGENTS AND

FILE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C2
CURRENT APPLICATION NUMBER: US/10/053.510
CURRENT FILING DATE: 2002-01-17
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 568
TYPE: PRN
ORGANISM: Mus musculus
US-10-053-510-6

Query Match 85.8%; Score 2553; DB 12; Length 568;
Best Local Similarity 84.1%; Pred. No. 4.8e-245;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWGEFV 60
DB 1 MPSTDLMLKDFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWYELI 60
QY 61 FQESLSMRKKKCFKTRKMPITGRKIODKLTNDISKNSFLKVDKEYKALPSQG 120
DB 61 FQESLSMRKKKFLKTRKMPITGRKIODKLTNDISKNSFLKVDKEYKALPSQG 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVYSGEKLTELKAYAGDFWANSPLHPIFPG 180
DB 121 MGTAEVLERKEYSSMDGSGWQEGKASGAVYNGEKLTELLVQAYGEFTWNSPLHPIFPG 180
QY 181 LRKLEAIVACISLFGNGDSCGCVTSGGTESTILMAKACRDLAEKGIKTEIVAPQS 240
DB 181 LRKLEAIVACISLFGNGDSCGCVTSGGTESTILMAKACRDLAEKGIKTEIVAPES 240
QY 241 AHAFAFNKAAAFYFGKIVRVLPTKMEYDVAMBRARISRNAMLVCSSTPQPHGVDPVE 300
DB 241 AHAFAFNKAAAFYFGKIVRVLPTKMEYDVAMBRARISRNAMLVCSSTPQPHGVDPVE 300
QY 301 VAKLAAYKIKPLHVDACLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLTAVRKIKPLHVDACLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSILVYSDKKRYNOFVDVDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
DB 361 SSIVVMSNEKRYNOFVDVDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
QY 421 KQIITKARFLKSELENKIFGVGNPQLSIALGSRDFDIYRLSNLTAGMNLNOQFP 480
DB 421 KQIITKARFLKSELENKIFGVGNPQLSIALGSRDFDIYRLSNLTAGMNLNOQFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
DB 481 RSIHFCITLVHTKRRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTIDRKLVAE 540
QY 541 LSSVFLDSLSTDTVTGSGOMNGSPKP 567
DB 541 ISSVFLDCLTYTDPVTGOMNGSPKP 567

RESULT 8
US-10-286-175-2
Sequence 2, Application US/10286175
Publication No. US2003005922A1
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington

COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/286.175
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Rosenman, Steven J.
REGISTRATION NUMBER: 43,058
REFERENCE/DOCKET NUMBER: 200116.402C3
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-286-175-2

Query Match 85.8%; Score 2553; DB 15; Length 568;
Best Local Similarity 84.1%; Pred. No. 4.8e-245;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWGEFV 60
DB 1 MPSTDLMLKDFEPYLEILEVYSTKAKNYNGHCTKEPQOLAMSVVMTLLVWYELI 60
QY 61 FQESLSMRKKKCFKTRKMPITGRKIODKLTNDISKNSFLKVDKEYKALPSQG 120
DB 61 FQESLSMRKKKFLKTRKMPITGRKIODKLTNDISKNSFLKVDKEYKALPSQG 120
QY 121 LSSAVLEKLEKESMDAFWQEGRASGVYSGEKLTELKAYAGDFWANSPLHPIFPG 180
DB 121 MGTAEVLERKEYSSMDGSGWQEGKASGAVYNGEKLTELLVQAYGEFTWNSPLHPIFPG 180
QY 181 LRKLEAIVACISLFGNGDSCGCVTSGGTESTILMAKACRDLAEKGIKTEIVAPQS 240
DB 181 LRKLEAIVACISLFGNGDSCGCVTSGGTESTILMAKACRDLAEKGIKTEIVAPES 240
QY 241 AHAFAFNKAAAFYFGKIVRVLPTKMEYDVAMBRARISRNAMLVCSSTPQPHGVDPVE 300
DB 241 AHAFAFNKAAAFYFGKIVRVLPTKMEYDVAMBRARISRNAMLVCSSTPQPHGVDPVE 300
QY 301 VAKLAAYKIKPLHVDACLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLTAVRKIKPLHVDACLGFLIVFMKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSILVYSDKKRYNOFVDVDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
DB 361 SSIVVMSNEKRYNOFVDVDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
QY 421 KQIITKARFLKSELENKIFGVGNPQLSIALGSRDFDIYRLSNLTAGMNLNOQFP 480
DB 421 KQIITKARFLKSELENKIFGVGNPQLSIALGSRDFDIYRLSNLTAGMNLNOQFP 480
QY 481 PSIHFCITLLHARKRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTVDNRNVAE 540
DB 481 RSIHFCITLVHTKRRAVIOFLKDIRESVTOIMKNPKAKTTGMAIYMAQTIDRKLVAE 540
QY 541 LSSVFLDSLSTDTVTGSGOMNGSPKP 567
DB 541 ISSVFLDCLTYTDPVTGOMNGSPKP 567

RESULT 9

US-10-197-073-10
: Sequence 10, Application US/10197073
: Publication No. US20030166897A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed Intellectual Property Law Group
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98055
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/197,073
: FILING DATE: 15-Jul-2002
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Urvater, Julie A.
: REGISTRATION NUMBER: 50,461
: REFERENCE/DOCKET NUMBER: 200116,402D2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-197-073-10

Query Match 83.9%; Score 2498; DB 12; Length 488;
Best Local Similarity 85.9%; Pred. No. 1,1e-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;
DB 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIYVGYEFV 60
1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIYVGYEFV 60
DB 61 FQPELSMSRFKKCKRKLTKRMPITGRKIDKLNKTDKDISKMSFLKYDKEYVKALPSQG 120
61 FQPELSMSRFKKCKRKLTKRMPITGRKIDKLNKTDKDISKMSFLKYDKEYVKALPSQG 120
DB 121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
DB 181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
DB 181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
DB 241 AHAANAKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVCSSTQPFPHGVDPPE 300
241 AHAANAKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVCSSTQPFPHGVDPPE 300
DB 301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
DB 301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
DB 361 SSVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISACWAALMHFGENGVEAT 420
361 SSVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISACWAALMHFGENGVEAT 420
DB 354 ----- 353

QY 421 KOIITAPRLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNOLOFP 480
DB 354 -----LENIKIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNOLOFP 400
QY 481 PSIHFCITLLHARKRAAIOFLKDIRESVQIKNPKAKTTGGATYMAQTVDNRMAVE 540
DB 401 PSIHFCITLLHARKRAAIOFLKDIRESVQIKNPKAKTTGGATYMAQTVDNRMAVE 460
QY 541 LSSVFLDSLSTDTVTYQGSOMNGSPKPH 568
DB 461 LSSVFLDSLSTDTVTYQGSOMNGSPKPH 488

RESULT 10
US-10-053-510-10
: Sequence 10, Application US/10053510
: Publication No. US20030175939A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: APPLICANT: Fyfe, Henrik
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: FILE REFERENCE: 200116,402C2
: CURRENT APPLICATION NUMBER: US/10/053,510
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 10
: LENGTH: 488
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-053-510-10

Query Match 83.9%; Score 2498; DB 12; Length 488;
Best Local Similarity 85.9%; Pred. No. 1,1e-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;
DB 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIYVGYEFV 60
1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHCTKYEPMQLIAMSVWTLTIYVGYEFV 60
DB 61 FQPELSMSRFKKCKRKLTKRMPITGRKIDKLNKTDKDISKMSFLKYDKEYVKALPSQG 120
61 FQPELSMSRFKKCKRKLTKRMPITGRKIDKLNKTDKDISKMSFLKYDKEYVKALPSQG 120
DB 121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
121 LSSSAVLEKLEKYSMDAFWQGRASGYVSGEEKLTLLVAYGDFAFMSNPLHDPDPG 180
DB 181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
DB 181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
181 LKRIAEIVRIACSLFNGPDSGCGVTSGETSILMACACADLAFKGIKTPETIAPAS 240
DB 241 AHAANAKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVCSSTQPFPHGVDPPE 300
241 AHAANAKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVCSSTQPFPHGVDPPE 300
DB 301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
DB 301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
301 VAKLAVKKRIPLHVACAGGLIVFMERAGYPLEHPDFRKGVSISADTHKYGAYAKG 360
DB 361 SSVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISACWAALMHFGENGVEAT 420
361 SSVLYSDKKYRNYQFVDTDMQGIYASPTIAGSRPGISACWAALMHFGENGVEAT 420
DB 354 ----- 353
QY 421 KOIITAPRLKSELENIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNOLOFP 480
DB 354 -----LENIKIGIFVGNPQLSLALGSRDPDIYRLSNLMTAKGNLNOLOFP 400
QY 481 PSIHFCITLLHARKRAAIOFLKDIRESVQIKNPKAKTTGGATYMAQTVDNRMAVE 540
DB 401 PSIHFCITLLHARKRAAIOFLKDIRESVQIKNPKAKTTGGATYMAQTVDNRMAVE 460

Db 401 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 460
QY 541 LSSVFLDSLXSTDTVTGSGOMNSPKPH 568
Db 461 LSSVFLDSLXSTDTVTGSGOMNSPKPH 488

RESULT 11

US-10-286-175-10
: Sequence 10, Application US/10286175
: Publication No. US2003005922A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
: METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Seed Intellectual Property Law Group
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98055
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/10/286.175
: FILING DATE: 30-Oct-2002
: CLASSIFICATION: <Unknown>
: ATTORNEY/AGENT INFORMATION:
: NAME: Roseman, Steven J.
: REGISTRATION NUMBER: 43,058
: REFERENCE/DOCKET NUMBER: 200116.402C3
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 662-6031
: INFORMATION FOR SEQ ID NO: 10:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 488 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
: SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-286-175-10

Query Match 83.9%; Score 2498; DB 15; Length 488;
Best Local Similarity 85.9%; Pred. No. 1.1e-239;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;
QY 1 MPSTDLMLKAFEPYILEVYSTAKANYNGHCTKYEPMOLIASVYVMTLLIYWGFEV 60
Db 1 MPSTDLMLKAFEPYILEVYSTAKANYNGHCTKYEPMOLIASVYVMTLLIYWGFEV 60
QY 61 FQPSLSMRKRCCKFKLTRKMPITIGRIQDKLTKDDISKNSFLKVDREYVNALPSOG 120
Db 61 FQPSLSMRKRCCKFKLTRKMPITIGRIQDKLTKDDISKNSFLKVDREYVNALPSOG 120
QY 121 LSSSAVLEKKEYSSMAFMOEGRASTVSGEKLTELIVKAYGDPANSNPLHPIFP 180
Db 121 LSSSAVLEKKEYSSMAFMOEGRASTVSGEKLTELIVKAYGDPANSNPLHPIFP 180
QY 181 LRKIEAIVRIACSLFNGCPDSCGCVSGTSTILMACACRDALFEKGIKTPETVAP 240
Db 181 LRKIEAIVRIACSLFNGCPDSCGCVSGTSTILMACACRDALFEKGIKTPETVAP 240
QY 241 AHAFAFNKASTFGMKIVRPLTKMVEDVVRAMRAISRNTAMLVCSPTQEPHGVDP 300
Db 241 AHAFAFNKASTFGMKIVRPLTKMVEDVVRAMRAISRNTAMLVCSPTQEPHGVDP 300

QY 301 VAKLAVKYPILPHVDAIGGLIYFMEKAGYPLEHPEDFRKGVTSIADTHKGYAPKG 360
Db 301 VAKLAVKYPILPHVDAIGGLIYFMEKAGYPLEHPEDFRKGVTSIADTHK----- 353
QY 361 SSLVYSDKKYRNYQFFVDTDWOGIYASPTIAGSRPGISACWALMHFGENGVEAT 420
Db 354 ----- 353
QY 421 KOITKARFLKSELENTKGFVGNPOLSLIAGSRPDIYRSLNLTAKGWLNOQFP 480
Db 354 -----LENTKGFVGNPOLSLIAGSRPDIYRSLNLTAKGWLNOQFP 400
QY 481 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 540
Db 401 PSIHFCITLLHARRKRAIOFLKDIRESVTOIMKNPKAKTTGMAIYMAOQTVDRNNVAE 460
QY 541 LSSVFLDSLXSTDTVTGSGOMNSPKPH 568
Db 461 LSSVFLDSLXSTDTVTGSGOMNSPKPH 488

RESULT 12

US-10-053-510-16
: Sequence 16, Application US/10053510
: Publication No. US20030175939A1
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Applicant: Fyfe, Henrik
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
: POLYNUCLEOTIDES AND MODULATING AGENTS AND
: TITLE OF INVENTION: METHODS OF USE THEREFOR
: FILE REFERENCE: 200116.402C2
: CURRENT APPLICATION NUMBER: US/10/053.510
: CURRENT FILING DATE: 2002-01-17
: NUMBER OF SEQ ID NOS: 21
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 16
: LENGTH: 545
: TYPE: PRT
: ORGANISM: Drosophila melanogaster
US-10-053-510-16

Query Match 45.1%; Score 1344; DB 12; Length 545;
Best Local Similarity 49.0%; Pred. No. 1.1e-124;
Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4;
QY 38 EPMOLIASVYVMTLLIYWGFEVFPQPSLSMRKRCCKFKLTRKMPITIGRIQDKLTKTD 97
Db 25 EPMQVATITATVTYLVGVMWMTVTCQDENLIRGKROFFKPAKIPARROVETELAKKN 84
QY 98 DISKNSFLKVDREYVNALPSOGIASSAVLEKKEYSSMAF-MQEGRASGYSGEKL 156
Db 85 DFEIEIKKSNALHTSETLPEKGLSKSEIIRLVDHLKTHGYMWRDRAVGAVGYKPD 144
QY 157 TELIVKAYGDPANSNPLHPIFPGLRIEAVIRIACSLFNGGSDSCGCVSGTSTILM 216
Db 145 VELTEVYGAASVTNPLHADLPFCVCKMEAEVVRAMCNLHNGSASCGMTGTGTSIVM 204
QY 217 ACKACRDALFE-KGIKTPETVAPQSAHAANAKASYGKIVRPL-TKMEVDRAMR 274
Db 205 AMKAYRFAREYKGITRPNIVPRTVHAADKGGQYNNIHVRSDVDPEYEVDIKKFR 264
QY 275 AISRNTAMLVCSPTQEPHGVIDVPEYVAKLAVKYPILPHVDAIGGLIYFMEKAGY 334
Db 265 AINRNTILVGSAPNFPYGTIDIDEALAGVYVDIPVHVDAIGGSFVALVHNAGYKL- 323
QY 335 HPDEFKRGVTSIADTHKGYAPKGSILVYSOKYRNYQFFVDTDWOGIYASPTIAG 394
Db 324 RPDEFKGVTSIADTHKGYAPKGSILVYSOKYKTDQFTYTDMPGCVGSGPTVNG 383
QY 395 SRPGISACWALMHFGENGVEATKOITKARFLKSELENTKGFVGNPOLSLIAG 454
Db 395 SRPGISACWALMHFGENGVEATKOITKARFLKSELENTKGFVGNPOLSLIAG 454

Db 384 SRAAGTIAACATMMSFGDGLYLRKRVDTARIENGVDIDGIFIFGKATSVIALG 443
Qy 455 SRDPDIYRLSNLTAKGNMNLQLOPPSIHFCITLLHARKRYAIOFLKDIRSVTOIMKN 514
Db 444 SVPDFIFRLSDSLCKLGNMNLQLOPPSGHLCVTDMHNPQGVADFIADVRSCTAIEIMKD 503
Qy 515 PRAKTTGKATYAMAQTTVDNRNMAELSSVFLDSLXT 552
Db 504 PQGPVYGMKALYGAQSIIPDRSVIGEVTRLFLHSMYTT 541

RESULT 13

US-10-053-510-11
; Sequence 11, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Fyfe, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053, 510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 552
; TYPE: PRF
; ORGANISM: C. elegans
US-10-053-510-11

Query Match 36.3%; Score 1082; DB 12; Length 552;
Best Local Similarity 42.7%; Pred. No. 1.4e-98;
Matches 228; Conservative 97; Mismatches 197; Indels 12; Gaps 7;

Qy 30 VNGHCTKYEPQOLI-----AMSVYVTLILVMGEYVFPQESLSRKKKCFKLRKMPITG 85
Db 22 INDRLSRYDPVYLVLAAGFGLVYTKV---HLYKRSDDPLLRMGAVYFSLRKLPAVR 78
Qy 86 RKIDOKLNTKDDISKMSFLKVDKEYVALPSOGSSAVLEKKEYSSMDAF-WQEGR 144
Db 79 DKIEKELAEKPKLIESIKDKDKOFISTLPRIAPDSISIELAKKYIEDYTFNIDGR 138
Qy 145 ASGTIVSGEE-KLTLLVYKAYGDFAMSNPLHPDIFPGRLKRIEATVIRIACSLFNGSPSC 203
Db 139 VSGAVYVTDHNAHINILGKIYEKAFNSNPLHPDVPFGAKMEALIRVNLNYGPEBDS 198
Qy 204 GCVTSGGTSTILMACKACDLAFEGKIKTPEIYVAFQSAHAFAFNKAASYFGMKIVKPLTK 263
Db 199 GSVTSGGTSTIIMAGFSYRNRAHSLGIEHPVILACKTAHAADFKAHLGCMELRHVPVDS 258
Qy 264 KMEVDVRAARAISRTAFLVCSFPOFPHGVIDPVEVAKLAVKYPILPHVACLGGLFI 323
Db 259 DNRVLDKEKMERLIDSNVCLVSAFNPFGSTIDPRLPIAKLCKTGIPYHVACLGGEPI 318
Qy 324 VMEKAGPPLFHPDFERKVGYSISADTHKYGARPGSSLVLYSDKKYRNYQFVYDTMQ 383
Db 319 PEMNAGY-LIIPVDFRNPQVTSISCDTHKYGCTPKGSSIVMYRSKELHHFGYFVADMC 377
Qy 384 GGTIVASPTAGSRPGISACWAALMHGPNQYVEATKQIITARFLKSELENINGIYF 443
Db 378 GGTIVASPTAGSRPGISACWAALMHGPNQYVEATKQIITARFLKSELENINGIYF 437
Qy 444 GNPOLSLALGSRDPIYRLSNLTAKGNMNLQLOPPSIHFCITLLHARKRYAIOFLKDIR 503
Db 438 GNSDVSIVAFSGNGNVIYFVSDKMKLGNMNLQLOPPSIHFCITLLHARKRYAIOFLKDIR 497
Qy 504 IRESVTQI-MKNPKAKTTGMAIYAMAQTTVDNRNMAELSSVFLDSLXTDTVT 556
Db 498 LKICEELAAKGEOKADSGMAAMYGA-AQVPSVYDEVIALYIDATYSAPST 550

RESULT 14

US-10-197-073-6
; Sequence 6, Application US/10197073
; Publication No. US20030166897A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Zhou, Jianhui
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LASE
; POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; METHODS OF USE THEREFOR

NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA

ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/197,073
FILING DATE: 15-Jul-2002
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Urvalter, Julie A.
REGISTRATION NUMBER: 50,461
REFERENCE/DOCKET NUMBER: 200116.402D2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 542 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 6:

US-10-197-073-6

Query Match 33.9%; Score 1008; DB 12; Length 542;
Best Local Similarity 38.1%; Pred. No. 3.2e-91;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

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Db 5 LEQYHS-ABDLIFELRKNPPLVLSSTIVATVYVLTNLRHMLHDEMGIKRLSTWFFTTV 63
Qy 79 RMPILIRKIDOKLNTKTRDDISKMSFLKVDKEYVALPSOGSSAVLEKKEYSSMDA 138
Db 64 KRVPIIRKIMDKQLNMEVDELEKSLRIYDRSTREYFTTIPSHSVGRTVLRALAIYDDLEG 123
Qy 139 -FWQGRASGIVYSGEELK--TELLVYKAYGDFAMSNPLHPDIFPGRLKRIEATVIRIACSL 195
Db 124 PAFLEGKRGVAGAFNEDEKDEREMVEEYVGAAMNPMPKLPFGVRIIMEAEVVMCCNM 183
Qy 196 FNGGPDGSCVNTSGGTSTILMACKACDLAFEGKIKTPEIYVAFQSAHAFAFNKAASYFGMK 255
Db 184 MNGDSETCGTMSTGSSISILLACLAHRNLRKRGKYTEMYIPSSVHAFAFKAACCFRIK 243
Qy 256 IYRVPLTKM-MEVDVRAARAISRTAFLVCSFPOFPHGVIDPVEVAKLAVKYPILPHV 314
Db 244 VKRIIVDPVTFKVDLVKKAAINRKTCLVGSAPNFPQGYDDIEAIGQLGLEYDIPVHV 303
Qy 315 DACLGGLIVMEKAGPPLFHPDFERKVGYSISADTHKYGARPGSSLVLYSDKKYRNY 374
Db 304 DACLGGLFLPFEED-----EIRYDPRVPGVSSISADSHKYGIAFGSSVLYLRNNKELAHN 359
Qy 375 QFVYDTMQGIGIYASPTAGSRPGISACWAALMHGPNQYVEATKQIITARFLKSEL 434

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Db 360 QYFCDDADMOGCIYASATWESSRAGHNIALCWAAMLVYHAQEGYKANARKIVDTTRKIRNGL 419
QY 435 ENIKGIFVFGNPNQSLIALGSRD-FDIYRLSNLTAKGWNLNQOPPSIHFCITLLHAR 493
Db 420 SNIKGIFLOGBSDVCISWTNDGVELXRFHNFMEKEKHQNLQFPAGVHIMVTMNH 479
QY 494 KRAVIOFLKDIRESVTQIM--KNPKAKTTGGAITYAMAQTTVDNRNVAELSSVFLDSL 551
Db 480 PGLAEAFVADOCRAAVEFVKSHKPSKSDTSEAIYGLAQSIPDRSLVHEFAHSYIDA 539
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RESULT 15

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US-10-053-510-4
; Sequence 4, Application US/10053510
; Publication No. US20030175939A1
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; APPLICANT: Eyrst, Henrik
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C2
; CURRENT APPLICATION NUMBER: US/10/053,510
; CURRENT FILING DATE: 2002-01-17
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: C. elegans
US-10-053-510-4
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Query Match 33.9%; Score 1008; DB 12; Length 542;

Best Local Similarity 38.1%; Pred. No. 3.2e-91;

Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

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Db 5 LEQYHS-AKDLLELFELKRFNPIVLSSTIATVLTNLRHMLDEMGIKRLSTWFTTV 63
QY 79 RKMPITGRKIODKLNKTKRDISKMSFLKYDKEYKALPSQGLSSAVLEKLEYSMDA 138
Db 64 KRVFPIRKMIDKQLENEKDELEKSLRIVDRSTEFYFTIPSHSVGRTEVLRLAAYDDEG 123
QY 139 -FMQEGRASCTVYSGEKL--TELLVKAQGFANSNPLHPIEPGLKITEAIVRIACSL 195
Db 124 PAFLEGRVSGAVFNRDEKDEREYEEVFGFAWNTNPLMPKLFPGVRIMEAEVVRMCCNM 183
QY 196 FNGGPDSCGCVTSQGTESILMACACRDLAFKGIKTPETIYAPQSAHAFAFKAAFGYGMK 255
Db 184 MNGDSEYCGTMTSGSISILLACLAHNRRLKRGKYTEMTIVPSSVHAFAFKAAECRIRK 243
QY 256 IVRVPLTKM-MEVDVRAAMRRAISRNTALVCSFPPHGVIDPVPEVAKLAVKXKPIPLHV 314
Db 244 VRKIPVDVPTFKVDLVKMKAIKRTCLMVGSAVNPFGVTVDIEAIGLGLEVDIPVHV 303
QY 315 DACLGGLIYMEKAGYPLEHPEDFRKYGTSISADTHKKYGAAPKSSLVLYSDKRYNY 374
Db 304 DACLGGLPLPLED---ELRYDFRVGVSSISADSHKYGGLAPKSSVLVYRNKELHN 359
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Db 360 QYPCDDADMOGCIYASATWESSRAGHNIALCWAAMLVYHAQEGYKANARKIVDTTRKIRNGL 419
QY 435 ENIKGIFVFGNPNQSLIALGSRD-FDIYRLSNLTAKGWNLNQOPPSIHFCITLLHAR 493
Db 420 SNIKGIFLOGBSDVCISWTNDGVELXRFHNFMEKEKHQNLQFPAGVHIMVTMNH 479
QY 494 KRAVIOFLKDIRESVTQIM--KNPKAKTTGGAITYAMAQTTVDNRNVAELSSVFLDSL 551
Db 480 PGLAEAFVADOCRAAVEFVKSHKPSKSDTSEAIYGLAQSIPDRSLVHEFAHSYIDA 539
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Search completed: October 6, 2003, 13:57:16
Job time : 42 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:46:54 ; Search time 25 Seconds
(without alignments)
961.303 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLLMLKAFPEYLEILE.....LYSDRYTQGSQMNNGSPKPH 568

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
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6: /cgn2_6/ptodata/2/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	US-08-939-309-4	Sequence 4, Appl1
2	2977	100.0	568	US-09-849-180-4	Sequence 4, Appl1
3	2977	100.0	568	US-09-356-643B-8	Sequence 8, Appl1
4	2959	99.4	568	US-09-238-373-2	Sequence 2, Appl1
5	2959	99.4	568	US-09-740-369-2	Sequence 2, Appl1
6	2553	85.8	568	US-08-939-309-2	Sequence 2, Appl1
7	2553	85.8	568	US-09-849-180-2	Sequence 2, Appl1
8	2553	85.8	568	US-09-356-643B-6	Sequence 6, Appl1
9	2498	83.9	488	US-08-939-309-10	Sequence 10, Appl1
10	2498	83.9	488	US-09-849-180-10	Sequence 10, Appl1
11	2498	83.9	488	US-09-356-643B-10	Sequence 10, Appl1
12	1082	36.3	552	US-09-356-643B-11	Sequence 11, Appl1
13	1008	33.9	542	US-08-939-309-6	Sequence 6, Appl1
14	1008	33.9	542	US-09-849-180-6	Sequence 6, Appl1
15	1008	33.9	542	US-09-356-643B-4	Sequence 4, Appl1
16	1007.5	33.8	589	US-08-939-309-8	Sequence 8, Appl1
17	1007.5	33.8	589	US-09-849-180-8	Sequence 8, Appl1
18	1007.5	33.8	589	US-09-356-643B-2	Sequence 2, Appl1
19	355	11.9	76	US-09-238-373-4	Sequence 4, Appl1
20	355	11.9	76	US-09-740-369-4	Sequence 4, Appl1
21	258.5	8.7	466	US-09-068-195-25	Sequence 25, Appl1
22	194	6.5	525	US-09-328-352-4492	Sequence 4492, Ap
23	155.5	5.2	502	US-09-114-001C-3598	Sequence 3598, Ap
24	148.5	5.0	489	US-09-134-001C-2920	Sequence 2920, Ap
25	144.5	4.9	398	US-09-328-352-4507	Sequence 4507, Ap
26	144	4.8	393	US-09-377-557-14	Sequence 14, Appl
27	137	4.6	583	5475086-4	Patent No. 5475086

28	131	4.4	584	1	US-08-161-290-1	Sequence 1, Appl1
29	131	4.4	584	2	US-08-450-755-1	Sequence 1, Appl1
30	131	4.4	585	1	US-08-117-907-2	Sequence 2, Appl1
31	131	4.4	585	1	US-08-485-718-11	Sequence 11, Appl1
32	131	4.4	585	1	US-08-485-718-13	Sequence 13, Appl1
33	131	4.4	585	2	US-08-484-530-57	Sequence 57, Appl1
34	131	4.4	585	2	US-08-484-530-59	Sequence 59, Appl1
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37	131	4.4	585	2	US-08-827-618A-57	Sequence 57, Appl1
38	131	4.4	585	3	US-08-483-952A-57	Sequence 57, Appl1
39	131	4.4	585	3	US-08-483-952A-59	Sequence 59, Appl1
40	131	4.4	585	3	US-08-483-952A-59	Sequence 59, Appl1
41	131	4.4	585	4	US-08-476-501-57	Sequence 57, Appl1
42	131	4.4	585	4	US-08-476-501-59	Sequence 59, Appl1
43	128	4.3	585	3	US-09-043-930-5	Sequence 5, Appl1
44	128	4.3	585	6	5475086-6	Patent No. 5475086
45	127.5	4.3	466	4	US-09-107-532A-4022	Sequence 4022, Ap

ALIGNMENTS

RESULT 1
US-08-939-309-4
; Sequence 4, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESSES:
; ADDRESS: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/939,309
; FILING DATE: 29-SEP-1997
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: David, Mark J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 200116,402
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 568 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-939-309-4

Query Match 100.0%; Score 2977; DB 4; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPSTDLLMLKAFPEYLEILEYSTRKAKYVNGHCKYEPWOLIAWSVYVTLIIWGYEFV 60
DB 1 MPSTDLLMLKAFPEYLEILEYSTRKAKYVNGHCKYEPWOLIAWSVYVTLIIWGYEFV 60

QY 61 QPESLMEFRKKCKTRKMPITGRKIDKLNKTDKSKNMSFLKVKREYKALPSSG 120
 Db 61 FQPESLMEFRKKCKTRKMPITGRKIDKLNKTDKSKNMSFLKVKREYKALPSSG 120
 QY 121 LSSSAVLEKLEKYSMDAFWQEGRASGVTVYSGEEKITELLVYKAGDFAWNP LHPDIFPG 180
 Db 121 LSSSAVLEKLEKYSMDAFWQEGRASGVTVYSGEEKITELLVYKAGDFAWNP LHPDIFPG 180
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 Db 181 LRKLEAEIVRIACSLFNGPGSCGCVTSGGTSSILMACACADLAEKGIKTPETIYAPOS 240
 QY 241 AHAAFNKAASTFGMKIVRPLTKMAEVDVRAARRAISRTAMLCVSTPOEPHGVIDPVE 300
 Db 241 AHAAFNKAASTFGMKIVRPLTKMAEVDVRAARRAISRTAMLCVSTPOEPHGVIDPVE 300
 QY 301 VAKLAVKXKIPLHVADCLGGFLIVEMEKAGYPLEHPDFRVRKGVTSISADTHKYGAPRG 360
 Db 301 VAKLAVKXKIPLHVADCLGGFLIVEMEKAGYPLEHPDFRVRKGVTSISADTHKYGAPRG 360
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 Db 361 SSLVLYSKKTRRNYEFVDTMOGGITVSPITAGSRPGCISAAACNALMHFGENGIVEAT 420
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 Db 421 KOIITTAFLKSELNINIGIFVFGNPNOLSLIAGSRDPIYRLSNMTAKGNLNOLOFP 480
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 Db 481 PSIHFCITLHARKKVAIQFLKDIRESVYQIMKNPKAKTTGAGATYAMAQTVVDRMVAE 540
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 Db 541 LSSVFLDSLSTDIYTGSGOMNGSPKPH 568

RESULT 2
 US-09-849-180-4
 Sequence 4, Application US/09849180
 Patent No. 6495359
 GENERAL INFORMATION:
 APPLICANT: Saba, Julie D.
 Zhou, Jianhui
 TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
 POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
 METHODS OF USE THEREFOR
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed Intellectual Property Law Group
 STREET: 701 Fifth Avenue, Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98055
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/849,180
 FILING DATE: 04-May-2001
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Pepe, Jeffrey C.
 REGISTRATION NUMBER: 46,985
 REFERENCE/DOCKET NUMBER: 200116.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 4:
 SEQUENCE CHARACTERISTICS:

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;      LENGTH: 568 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 4:
us-09-849-180-4

Query Match      100.0%; Score 2977; DB 4; Length 568;
Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0

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Db 1 MPSTDLMLKAFEPLEILEVYSTAKNVVGNCHCTYPEPMOLIASVYVTLTIIVGVEFV 60
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Db 181 LRKTEAEIVRACSLFENGSPDSCGCVTSGGTGSTIMACKACRDLAEFGIKTPEIVAPQS 240
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OY 301 VAKLAVKKIPLHADACLGGLIYFMEKAGTPLEHPDFRKYKCVTSISADTHKTYAPRG 360
Db 301 VAKLAVKKIPLHADACLGGLIYFMEKAGTPLEHPDFRKYKCVTSISADTHKTYAPRG 360
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Db 361 SSLVLSYSKKTRNIOFVDTDMOGGIVASPTTAGSRPGISACAAALMHRENGEYVET 420
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Db 421 KOIKTARFLSELENIGIYFVFGNPQSLIALGSRDEDIYRLSNMTRAKGNLNLQLOFP 480
OY 481 PSIHFCITLHARRKVAIQFLKDIRESVTOIMKNPKAKTTGGKAIYAMAQTTVDRNVAE 540
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Db 541 LSSVFLDSLSTDPVYTOGSGMNGSPKPH 568

RESULT 3
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; Sequence 8, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356.643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 568
; TYPE: PRT
; ORGANISM: Homo sapiens
us-09-356-643B-8

Query Match      100.0%; Score 2977; DB 4; Length 568;

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Best Local Similarity 100.0%; Pred. No. 2,7e-279;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MPSTDLMLKAFEPYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60
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Db 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSFLKVDKEYVALPSQG 120
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Db 301 VAKLAVKXKIPLHVADACLGFLYFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
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Db 421 KOIKTARFLKSELENKIGIFVFGNPOLSLIALSRODPIYRLSNLMTAKMNLNOLOFP 480
OY 481 PSIHFCITLLHARRRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYAMAQTTVDNRNVAE 540
Db 481 PSIHFCITLLHARRRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYAMAQTTVDNRNVAE 540
OY 541 LSSVFLDSLXYSTDTVTGQSQMNGSPKPH 568
Db 541 LSSVFLDSLXYSTDTVTGQSQMNGSPKPH 568
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RESULT 4

US-09-238-373-2
: Sequence 2, Application US/09238373A
: Patent No. 6187562
: GENERAL INFORMATION:
: APPLICANT: DUCKWORTH, DAVID MALCOLM
: APPLICANT: GODDEN, ROBERT JAMES
: APPLICANT: TESTA, TANIA TAMSON
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30034
: CURRENT APPLICATION NUMBER: US/09/238, 373A
: CURRENT FILING DATE: 1999-01-27
: EARLIER APPLICATION NUMBER: UK 9824026.0
: EARLIER FILING DATE: 1998-11-03
: EARLIER APPLICATION NUMBER: EP 98300625.5
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 2
: LENGTH: 568
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-238-373-2

Query Match 99.4%; Score 2959; DB 3; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.5e-277;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60

Db 1 MPSTDLMLKAFEPYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60

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OY 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSFLKVDKEYVALPSQG 120
Db 61 FQPELSLRFKKKCFKTLRKMPITIGRKIODKLNKTODISKNSFLKVDKEYVALPSQG 120
OY 121 LSSSAVLEKLEYSMDAFMOEGRASGVYSGEEKLTLLKAYGDFAMSNPLHPDIFPG 180
Db 121 LSSSAVLEKLEYSMDAFMOEGRASGVYSGEEKLTLLKAYGDFAMSNPLHPDIFPG 180
OY 181 LKRIEATVRIACSLFNGSPDSCGCVTSGGESTILMACKACRDIAFEKGIKTPETIVAPQS 240
Db 181 LKRIEATVRIACSLFNGSPDSCGCVTSGGESTILMACKACRDIAFEKGIKTPETIVAPQS 240
OY 241 AHAFAFNKAASYFGMKIVRVPLTKMMEVDVRRAMRAISRNTAMLVCSIPQPFHGYIDPVE 300
Db 241 AHAFAFNKAASYFGMKIVRVPLTKMMEVDVRRAMRAISRNTAMLVCSIPQPFHGYIDPVE 300
OY 301 VAKLAVKXKIPLHVADACLGFLYFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
Db 301 VAKLAVKXKIPLHVADACLGFLYFMEKAGYPLEHPDFRVKGYTSSADTHKKGYAPKG 360
OY 361 SSLVLYSDKKYRNQOFVDTDMOGGIYASPTIAGSRPGISAAACWALMHFGNGYVEAT 420
Db 361 SSLVLYSDKKYRNQOFVDTDMOGGIYASPTIAGSRPGISAAACWALMHFGNGYVEAT 420
OY 421 KOIKTARFLKSELENKIGIFVFGNPOLSLIALSRODPIYRLSNLMTAKMNLNOLOFP 480
Db 421 KOIKTARFLKSELENKIGIFVFGNPOLSLIALSRODPIYRLSNLMTAKMNLNOLOFP 480
OY 481 PSIHFCITLLHARRRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYAMAQTTVDNRNVAE 540
Db 481 PSIHFCITLLHARRRVAIOFLKDIRESVTQIMKNPKAKTTGMAIYAMAQTTVDNRNVAE 540
OY 541 LSSVFLDSLXYSTDTVTGQSQMNGSPKPH 568
Db 541 LSSVFLDSLXYSTDTVTGQSQMNGSPKPH 568
```

RESULT 5

US-09-740-369-2
: Sequence 2, Application US/09740369
: Patent No. 6521437
: GENERAL INFORMATION:
: APPLICANT: DUCKWORTH, DAVID MALCOLM
: APPLICANT: GODDEN, ROBERT JAMES
: APPLICANT: TESTA, TANIA TAMSON
: TITLE OF INVENTION: NOVEL COMPOUNDS
: FILE REFERENCE: GP-30034-D1
: CURRENT APPLICATION NUMBER: US/09/740, 369
: CURRENT FILING DATE: 2000-12-19
: PRIOR APPLICATION NUMBER: EP 98300625.5
: PRIOR FILING DATE: 1998-01-29
: PRIOR APPLICATION NUMBER: UK 9824026.0
: PRIOR FILING DATE: 1998-11-03
: PRIOR APPLICATION NUMBER: 09/238, 373
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 568
: TYPE: PRT
: ORGANISM: HOMO SAPIENS
US-09-740-369-2

Query Match 99.4%; Score 2959; DB 4; Length 568;
Best Local Similarity 99.5%; Pred. No. 1.5e-277;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNYVGHCTKYEPMQLIAMSVVWTLIIWGYEFV 60

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OY      61  QPESLWRFKKCKELTRKMPITIGRTIODKLNTKRDJSTKMSFLKYK EYVKALPSOG 120
Db      61  FQPSLWRFKKCKELTRKMPITIGRTIODKLNTKRDJSTKMSFLKYK EYVKALPSOG 120
OY      121 LSSSAVLEKLEKEYSSMDAFWQEGRASCTVYSGCEKLTLELLVYAGDGFAMSNPLHPDIFPG 180
Db      121 LSSSAVLEKLEKEYSSMDAFWQEGRASCTVYSGCEKLTLELLVYAGDGFAMSNPLHPDIFPG 180
OY      181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACACADLAFEKGIKTPETIYAPDS 240
Db      181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACACADLAFEKGIKTPETIYAPDS 240
OY      241 AAHAFNKAASFEGMIVRPLTKMMEVDVRAARRAISRTTALMVSTPOEPFGVIDPVE 300
Db      241 AAHAFNKAASFEGMIVRPLTKMMEVDVRAARRAISRTTALMVSTPOEPFGVIDPVE 300
OY      301 VAKLAVKKYKPIPLHADCLGGLFIVEMERAGYPLDHPDFRVAKVTSISADTHKKYGAPKG 360
Db      301 VAKLAVKKYKPIPLHADCLGGLFIVEMERAGYPLDHPDFRVAKVTSISADTHKKYGAPKG 360
OY      361 SSLVLYSKKTRNVOFEVDTMOGSIYASPTIAGSRPGISAAACMAALHFGENGVEAT 420
Db      361 SSLVLYSKKTRNVOFEVDTMOGSIYASPTIAGSRPGISAAACMAALHFGENGVEAT 420
OY      421 KOIITARFELKSELENIGIFVFGNPOLSLILGSRDFIYRLSNLTAKGNLNOLOP 480
Db      421 KOIITARFELKSELENIGIFVFGNPOLSLILGSRDFIYRLSNLTAKGNLNOLOP 480
OY      481 PSIHFCITLLHARKRVAIQFLKDIRESVTQIMKNPRAKTTGGAITYAMAQTVDRNMVAE 540
Db      481 PSIHFCITLLHARKRVAIQFLKDIRESVTQIMKNPRAKTTGGAITYAMAQTVDRNMVAE 540
OY      541 LSSVFLDLSYSTDVTQSGQNMNGSRKH 568
Db      541 LSSVFLDLSYSTDVTQSGQNMNGSRKH 568

RESULT 6
US-08-939-309-2
: Sequence 2, Application US/08939309
: Patent No. 6423527
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: APPLICANT: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
: TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
: NUMBER OF INVENTION: METHODS OF USE THEREFOR
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED AND BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/939,309
: FILING DATE: 29-SEP-1997
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: David, Mark J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/DOCKET NUMBER: 200116.402
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 2:

```

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: SEQUENCE CHARACTERISTICS:
: LENGTH: 568 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
us-08-939-309-2

Query Match 85.8%; Score 2553; DB 4; Length 568;
Best Local Similarity 84.1%; Pred. No. 36-228;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

OY 1 MPSTDLMLKAFEPYLELLEIVSTKAKNVNGHCTKREPMOLIANSVVTLIIWGYEYF 60
DB 1 MPGLDILKLPPEPYLELLEISTYKAKNVNGCYCKREPMOLIANSVLCTLLIIVWYELI 60
OY 61 FQPELSMRFKKCKKLTTRKMPITGRKTODKLNTKDKDISKMSLEKVDKEYKALPSQG 120
DB 61 FQPELSMRFKKCKKLTTRKMPITGRKTIEQVSKAKKDLVKMMPLEKVDKYKTLPAQG 120
OY 121 LSSAVLEKLEKLEYSMDAFWQGRASGVYSEEEKLTLLVAYADPMANPLHDPDIFG 180
DB 121 MGTAVLELERLEKLEYSMDGSKASGAYYNEPKLTLLVQAYGEFTWSNPLHDPDIFG 180
OY 181 LRKIAEIVLRACSLFNGGPDSCGCVTSQGTESIIMACKACDLAFKGIKTPETIAPQS 240
DB 181 LRKIAEIVLRACSLFNGGPDSCGCVTSQGTESIIMACKACDLALDKGIKTPETIAPQS 240
OY 241 AHAENKASVFGMKIVRVLTKMMEVDVRAARRAISRTAMLVGSTPQFPHGVDPVPE 300
DB 241 AHAEDKAAHFGMKIVRVALKKNMEVDVQAKRAISRNTAMLVGSTPQFPHGVMDPVPE 300
OY 301 VAKLAVKKRPIPLHVACAGLGLIIVMEKAGVLEHPDFDRVGVGVSISADTKHYGAPKG 360
DB 301 VAKLTVRKPIPLHVACAGLGLIIVMEKAGVLEKPEFDRVGVGVSISADTKHYGAPKG 360
OY 361 SSVLYSKKKRYNTQFVYDIDMQGIVYASPTIAGSRPGISAAACNALHFGENGVEAT 420
DB 361 SSVVYMSNEKRYTYFPGADWDQGVYASPTIAGSRPGIIMACNALHFGENGVEAT 420
OY 421 KOIITARFLESELENIKIGIEVFGNPQLSLALGSRDPDIYRLSLMTAKGNLQLOFP 480
DB 421 KOIITARFLESELENIKIFIFGDPQLSVIALGSDNFDIYRLSNMMSAKGNFNLYLOFP 480
OY 481 PSIHFCITLLHARRKVAIOFLKDIRESVQIIMKNKRAKTGTGAIYAMQTVDRMVAE 540
DB 481 RSIHFCITLVHRRKVAIOFLKDIRESVQIIMKNKRAKTGTGAIYAMQATVDRKVAE 540
OY 541 LSSVFLDSLYSTDTVTOGSONGSPKP 567
DB 541 ISSVFLDCLYTTDPVTOGNONGSPKP 567

RESULT 7
US-09-849-180-2
: Sequence 2, Application US/09849180
: Patent No. 6495359
: GENERAL INFORMATION:
: APPLICANT: Saba, Julie D.
: Zhou, Jianhui
: TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
:
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESS: Seed Intellectual Property Law Group
: STREET: 701 Fifth Avenue, Suite 6300
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: floppy disk
: COMPUTER: IBM PC compatible

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 568 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-849-180-2

Query Match 85.8%; Score 2553; DB 4; Length 568;
Best Local Similarity 84.1%; Pred. No. 3e-238;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAPPEYLEILEVYSTKAKNYNGHCTKTEPQOLAMSVVTLTVMGYEFV 60
DB 1 MPSTDLMLKDEPEYLEILESTYKAKNYNGCTKTEPQOLAMSVLCTLLVWYELI 60
QY 61 FQESLMSRKKKCFKLTTRKMPITGRKIODLKNKTDDISKNSFLKVDKEYKALPSQG 120
DB 61 FQESLMSRKKKFLTKIRKMPITGRKIEQVSKAKKDLVKNMPLKVDYKTLPAQG 120
QY 121 LSSAVLEKLEKSSMDAFQEGRASGVYSGEEKLTLLVKAAGDPANPLHPDIFPG 180
DB 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
QY 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
DB 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
QY 181 LRLEAEIVAMTCSLNGGDSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 240
DB 181 LRLEAEIVAMTCSLNGGDSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 240
QY 241 AHAFAFKAAHYFGMKIVRAALKKMEVDVQAMKRAISRNTAMLCSTPQPHGVMDVPE 300
DB 241 AHAFAFKAAHYFGMKIVRAALKKMEVDVQAMKRAISRNTAMLCSTPQPHGVMDVPE 300
QY 301 VAKLAVKYYKIPLVHVDACLGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKYYKIPLVHVDACLGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVVMTSNEKRYRQFFVGADMGVYASPSIAGSRGGITAAACMAALHFGENGVEAT 420
DB 361 SSVVMTSNEKRYRQFFVGADMGVYASPSIAGSRGGITAAACMAALHFGENGVEAT 420
QY 421 KQIKTARFLKSELENIKIGFVGNPOLSLIALGSDFDIYRLSNLTAKGMLNLOLQFP 480
DB 421 KQIKTARFLKSELENIKIFIGDPOLSVIALGSDFDIYRLSNMMSAKGMNFNLOLQFP 480
QY 481 PSIHFCITLLHAKKRAVIOFLKDIRSVTOIMKNPRAKTGTGMAIYAMAQTVDRNVAE 540
DB 481 PSIHFCITLVHTKRAVIOFLKDIRSVTOIMKNPRAKTGTGMAIYAMAQTVDRNVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONGSPKP 567

RESULT 8
US-09-356-643B-6
Sequence 6, Application US/09356643B
Patent No. 6569666
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.

TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
FILE REFERENCE: 200116.402C1
CURRENT APPLICATION NUMBER: US/09/356,643B
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 6
LENGTH: 568
TYPE: PRT
ORGANISM: Mus musculus
US-09-356-643B-6

Query Match 85.8%; Score 2553; DB 4; Length 568;
Best Local Similarity 84.1%; Pred. No. 3e-238;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAPPEYLEILEVYSTKAKNYNGHCTKTEPQOLAMSVVTLTVMGYEFV 60
DB 1 MPSTDLMLKDEPEYLEILESTYKAKNYNGCTKTEPQOLAMSVLCTLLVWYELI 60
QY 61 FQESLMSRKKKCFKLTTRKMPITGRKIODLKNKTDDISKNSFLKVDKEYKALPSQG 120
DB 61 FQESLMSRKKKFLTKIRKMPITGRKIEQVSKAKKDLVKNMPLKVDYKTLPAQG 120
QY 121 LSSAVLEKLEKSSMDAFQEGRASGVYSGEEKLTLLVKAAGDPANPLHPDIFPG 180
DB 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
QY 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
DB 121 LSSAVLEKLEKSSMDQSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 180
QY 181 LRLEAEIVAMTCSLNGGDSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 240
DB 181 LRLEAEIVAMTCSLNGGDSGCVYSGESTILMACRACRDALAEKGTPEIYAPES 240
QY 241 AHAFAFKAAHYFGMKIVRAALKKMEVDVQAMKRAISRNTAMLCSTPQPHGVMDVPE 300
DB 241 AHAFAFKAAHYFGMKIVRAALKKMEVDVQAMKRAISRNTAMLCSTPQPHGVMDVPE 300
QY 301 VAKLAVKYYKIPLVHVDACLGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
DB 301 VAKLAVKYYKIPLVHVDACLGGLIVFMEKAGYPLEHPDFRVKGVTSISADTHKYGAPKG 360
QY 361 SSVVMTSNEKRYRQFFVGADMGVYASPSIAGSRGGITAAACMAALHFGENGVEAT 420
DB 361 SSVVMTSNEKRYRQFFVGADMGVYASPSIAGSRGGITAAACMAALHFGENGVEAT 420
QY 421 KQIKTARFLKSELENIKIGFVGNPOLSLIALGSDFDIYRLSNLTAKGMLNLOLQFP 480
DB 421 KQIKTARFLKSELENIKIFIGDPOLSVIALGSDFDIYRLSNMMSAKGMNFNLOLQFP 480
QY 481 PSIHFCITLLHAKKRAVIOFLKDIRSVTOIMKNPRAKTGTGMAIYAMAQTVDRNVAE 540
DB 481 PSIHFCITLVHTKRAVIOFLKDIRSVTOIMKNPRAKTGTGMAIYAMAQTVDRNVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONGSPKP 567

RESULT 9
US-08-939-309-10
Sequence 10, Application US/08939309
Patent No. 6423527
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
TITLE OF INVENTION: POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
TITLE OF INVENTION: METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/939,309
FILING DATE: 29-SEP-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: David, Maki J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-939-309-10

Query Match 83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MSTDLIMKAEPEYLEILEVYSTAKNVNGCHTKYEPWOLIAMSVVWTLIIWGYEFV 60
DB 1 MSTDLIMKAEPEYLEILEVYSTAKNVNGCHTKYEPWOLIAMSVVWTLIIWGYEFV 60
QY 61 FQPELSMSRFKKCKRKLTRKMPITIGRKIDDKLNTKDDISKNMFLKVDKEYKALPSSG 120
DB 61 FQPELSMSRFKKCKRKLTRKMPITIGRKIDDKLNTKDDISKNMFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFPG 180
QY 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGETSILMACACRDLAFEGIKTPEIYAPQS 240
DB 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGETSILMACACRDLAFEGIKTPEIYAPQS 240
QY 241 AHAENKKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVGSTPQFPFGVIDPYPE 300
DB 241 AHAENKKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVGSTPQFPFGVIDPYPE 300
QY 301 VAKLAVKKKIPLHVDACLGGLIIVEMEKAGYLEHPDFRVKGVTSISADTHKYGAPRG 360
DB 301 VAKLAVKKKIPLHVDACLGGLIIVEMEKAGYLEHPDFRVKGVTSISADTHKYGAPRG 360
QY 361 SSVLYSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYVEAT 420
DB 361 SSVLYSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYVEAT 420
QY 421 KOITARFLKSELENIKGIFVFGNPOLSLIAGSRDPDIYPLSLNMTAKGNLQLOFP 480
DB 421 KOITARFLKSELENIKGIFVFGNPOLSLIAGSRDPDIYPLSLNMTAKGNLQLOFP 480
QY 481 PSIHFCITLLHARKKVAIOFLKDIRESYTOIKMKNRAKTGTGALYAAOQTVDRNVAE 540
DB 481 PSIHFCITLLHARKKVAIOFLKDIRESYTOIKMKNRAKTGTGALYAAOQTVDRNVAE 540
QY 541 LSSVFLDSLSTDTVTGSGQNMNGSPKPH 568
DB 541 LSSVFLDSLSTDTVTGSGQNMNGSPKPH 568
QY 568 LSSVFLDSLSTDTVTGSGQNMNGSPKPH 568
DB 568 LSSVFLDSLSTDTVTGSGQNMNGSPKPH 568

RESULT 10
US-09-849-180-10
Sequence 10, Application US/09849180
Patent No. 6495359
GENERAL INFORMATION:
APPLICANT: Saba, Julie D.
TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE
POLYPEPTIDES, POLYNUCLEOTIDES AND MODULATING AGENTS AND
METHODS OF USE THEREFOR
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed Intellectual Property Law Group
STREET: 701 Fifth Avenue, Suite 6300
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98055
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/849,180
FILING DATE: 04-May-2001
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pepe, Jeffrey C.
REGISTRATION NUMBER: 46,985
REFERENCE/DOCKET NUMBER: 200116.402
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-849-180-10

Query Match 83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

QY 1 MSTDLIMKAEPEYLEILEVYSTAKNVNGCHTKYEPWOLIAMSVVWTLIIWGYEFV 60
DB 1 MSTDLIMKAEPEYLEILEVYSTAKNVNGCHTKYEPWOLIAMSVVWTLIIWGYEFV 60
QY 61 FQPELSMSRFKKCKRKLTRKMPITIGRKIDDKLNTKDDISKNMFLKVDKEYKALPSSG 120
DB 61 FQPELSMSRFKKCKRKLTRKMPITIGRKIDDKLNTKDDISKNMFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGVYSGEEKITELLVAKYAGDFAMSNPLHDPFPG 180
QY 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGETSILMACACRDLAFEGIKTPEIYAPQS 240
DB 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGETSILMACACRDLAFEGIKTPEIYAPQS 240
QY 241 AHAENKKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVGSTPQFPFGVIDPYPE 300
DB 241 AHAENKKAASYFGMKIVRPLTKMMEVDVRAARRAISRTAMLVGSTPQFPFGVIDPYPE 300
QY 301 VAKLAVKKKIPLHVDACLGGLIIVEMEKAGYLEHPDFRVKGVTSISADTHKYGAPRG 360
DB 301 VAKLAVKKKIPLHVDACLGGLIIVEMEKAGYLEHPDFRVKGVTSISADTHKYGAPRG 360
QY 361 SSVLYSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYVEAT 420
DB 361 SSVLYSDKKYRNYPFVDTMOGGIYASPTIAGSRPGISAAACMAALMHFGENGYVEAT 420


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Db      354 ----- 353
QY      421 KOIKTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGWNLOQFP 480
Db      354 -----LENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGWNLOQFP 400
QY      481 PSIHFCITLLHARKRAVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTTVDNRNVAE 540
Db      401 PSIHFCITLLHARKRAVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTTVDNRNVAE 460
QY      541 LSSVFIDSLYSTDTVTQGSOMNGSPKPH 568
Db      461 LSSVFIDSLYSTDTVTQGSOMNGSPKPH 488

RESULT 11
US-09-356-643B-10
; Sequence 10, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 488
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-356-643B-10

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Query Match      83.9%; Score 2498; DB 4; Length 488;
Best Local Similarity 85.9%; Pred. No. 4.9e-233;
Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1;

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QY      1 MSTDLMLKAPPEYLEILEVYSTKAKNVNCHCTYEPPQOLANSVWTLTVMGYEFV 60
Db      1 MSTDLMLKAPPEYLEILEVYSTKAKNVNCHCTYEPPQOLANSVWTLTVMGYEFV 60
QY      61 POPESLMSRFKKCKFLTRKMPITIGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSOG 120
Db      61 POPESLMSRFKKCKFLTRKMPITIGRKIDKLKTKDIDSKNMSFLKVDKEYKALPSOG 120
QY      121 LSSSAVLEKLEKYSMDAFWQEGRASGTYVSGEKLTELLVKAAGDFPANSNPLHPDIFPG 180
Db      121 LSSSAVLEKLEKYSMDAFWQEGRASGTYVSGEKLTELLVKAAGDFPANSNPLHPDIFPG 180
QY      181 LKRIEIEIYRIACSLNENGPDSGCVTSSTGESILMACACRDLAEKGIKTEIYIAPQS 240
Db      181 LKRIEIEIYRIACSLNENGPDSGCVTSSTGESILMACACRDLAEKGIKTEIYIAPQS 240
QY      241 AHAFAFKKASYSFGMKIVRPVLTAKMEVDVYRAMRRASRTAMLVCTPOPHGVIPVPE 300
Db      241 AHAFAFKKASYSFGMKIVRPVLTAKMEVDVYRAMRRASRTAMLVCTPOPHGVIPVPE 300
QY      301 VAKLAVKXKIPLHVDAICGLFVLEMEKAGYPLEHPDFRKYKVTISADTHKYYAPKG 360
Db      301 VAKLAVKXKIPLHVDAICGLFVLEMEKAGYPLEHPDFRKYKVTISADTHKYYAPKG 360
QY      361 SSVLYLXSDKKRYRYOFVVDMDQGGIYASPTINGSPGGISAAACMAALMHFGNGYEAT 420
Db      354 ----- 353
QY      421 KOIKTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGWNLOQFP 480
Db      354 -----LENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGWNLOQFP 400
QY      481 PSIHFCITLLHARKRAVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTTVDNRNVAE 540

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Db      401 PSIHFCITLLHARKRAVAIOFLKDIRSVTOIMKNPRAKTTGMAIYAMAQTTVDNRNVAE 460
QY      541 LSSVFIDSLYSTDTVTQGSOMNGSPKPH 568
Db      461 LSSVFIDSLYSTDTVTQGSOMNGSPKPH 488

RESULT 12
US-09-356-643B-11
; Sequence 11, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356,643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 552
; TYPE: PRF
; ORGANISM: C. elegans
US-09-356-643B-11

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Query Match      36.3%; Score 1082; DB 4; Length 552;
Best Local Similarity 42.7%; Pred. No. 6.8e-96;
Matches 228; Conservative 97; Mismatches 197; Indels 12; Gaps 7;

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QY      30 VNGCHCTYEPPQOLI-----ANSVWTLTVMGYEFVPOPESLMSRFKKCKFLTRKMPITIG 85
Db      22 INDRLSRYPDVVLVLAFGGTLVYTKV---HLIKSEDPILRMGAIVYSLRKLPAYR 78
QY      86 RKIDKLKTKDIDSKNMSFLKVDKEYKALPSOGILSSSAVLEKLEKYSMDAF-WQEGR 144
Db      79 DRIEKLAEKPKLIESIHHDKQOFISTPLIAPLSODSIMELAKKEDYFNFNINDGR 138
QY      145 ASGTIVSGEE-KTELLVYRAYGDFPANSNPLHPDIFPGCLKRIEIEIYRIACSLNENGPDSG 203
Db      139 VSGAVYTDRAHEHINILGKIYERKAFSNPLHPDIFPGARMEMELLRMYLNLNENGPDS 198
QY      204 GCVTSSTGESILMACACRDLAEKGIKTEIYIAPQSAHAFAFKKASYSFGMKIVRPVLT 263
Db      199 GSVTSSTGESITACSYRRRAHSLGTEHPIIACCTAAAFKAAHLGMRRLRHPVDS 258
QY      264 MMEVDVYRAMRRASRTAMLVCTPOPHGVIPVPEVAKLAVKXKIPLHVDAICGLF 323
Db      259 DNRVLEKEMRLIDSNVCMVGSAPNPPSGTIDPIELAKLGKKGIPVHVDAICGLFMI 318
QY      324 VFEKAGYPLEHPDFRKYKVTISADTHKYYAPKGSSSVLYLXSDKKRYRYOFVVDMDQ 383
Db      319 PFNMDAGY-LIPFEDRNPNPVTISCDTHKYYGCTPGKSSIVMYRSEKLHFOFESVADMC 377
QY      384 GGIVASPTINGSPGGISAAACMAALMHFGNGYEATKOIKTARFLKSELENIKGFV 443
Db      378 GGIVATPTINGSPAGANTAYAMAATLLSFGDEYVRCQAQYKTRMLAEIKIKTKPY 437
QY      444 GNPOLSLIALGSRDPDIYRLSNLMTAKGWNLOQFPSPSIHFICITLLHARKRAVAIOFLK 503
Db      438 GKSDVSLVAFSGNGVNIYEVSDKMKLGNLNTLPQPAATHICLTINQANEEVVAFAVD 497
QY      504 IRESYVOI-WKNPRAKTTGMAIYAMAQTTVDNRNVAELSSVFLDSIXSDIYT 556
Db      498 LEKICELELAKGQAKADSGMAAMYGMA-AQVPRSVDEVETALYIDATYSAAPST 550

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RESULT 13
US-08-939-309-6
; Sequence 6, Application US/08939309
; Patent No. 6423527
; GENERAL INFORMATION:

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Db 304 DACIGFELPFLEED---EIRYDFRPVSSISADSHKXGLAPKSSVLYRKKELJHN 359
Qy 375 QEFVVDMDMGITASPTIAGSRPGISAAACALMHGEGYEATQIITKTAFLKSEL 434
Db 360 QYFCDDMGGITASATMGSRAHNTALCWAALYHAQEGYANARKIVDTTRKIRNGL 419
Qy 435 ENIKGIFVFGNPNOLSLALGSRD-FDIYRLSNLMTAKGWNLNOLQPPSIHFCITLLHAR 493
Db 420 SNIKGIRKLGSPDVCISWNTNGVELYRPHNEMKEKHMQLNGIQFPAGHIMVTMHTH 479
Qy 494 KRAVIOFLKDIRSVTQIM--KNPKAKTGMGAITYAMAQTVDNRNVAELSSVFLDSLVS 551
Db 480 PGLAEAFVADCRAAVEFVKSHKPSSEDKTSEAAIYGLAQSIIPDRSLVHEFAHSYIDAVYA 539

RESULT 15
US-09-356-643B-4
; Sequence 4, Application US/09356643B
; Patent No. 6569666
; GENERAL INFORMATION:
; APPLICANT: Saba, Julie D.
; TITLE OF INVENTION: SPHINGOSINE-1-PHOSPHATE LYASE POLYPEPTIDES,
; TITLE OF INVENTION: POLYNUCLEOTIDES AND MODULATING AGENTS AND
; TITLE OF INVENTION: METHODS OF USE THEREFOR
; FILE REFERENCE: 200116.402C1
; CURRENT APPLICATION NUMBER: US/09/356.643B
; CURRENT FILING DATE: 1999-07-19
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ. ID NO 4
; LENGTH: 542
; TYPE: PRT
; ORGANISM: C. elegans
US-09-356-643B-4

Query Match 33.9%; Score 1008; DB 4; Length 542;
Best Local Similarity 38.1%; Pred. No. 9.6e-89;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;
Qy 19 LEVYSTAKNYVNGHCTKYRPMOLIANVYWTLLIYGYEVPFOPESLMSRFKKCKPKLT 78
Db 5 LEQYHS-AKDLLIFELRKFNPIVLSSTIVATVTLNLRHMHLEDMGIRKRLSTWFETTV 63
Qy 79 RKMPIIGRKIQDILNKTKDIDISKNMSFLKYDKYKALPSQGLSSAVLEKIKESMDA 138
Db 64 KRVPFIRKMTDKOLNEVKDELKSLRIVDRSTFETTPSHSVGRTEVLRILAAYIDDEG 123
Qy 139 -FWQGRASGTYSGEEL--TELLVAYGDFAMSNLHPDIFPGLRIEAEIYRIACSL 195
Db 124 PAFLGKAVSGAVNREDDKEREYEFKFAFNTNIMPKLPPGVAIMAEVYRMCCNM 183
Qy 196 FNGPDSGCVTSGGTESIIMACKACHDLAFEGIKTPETIYAPQSAHAFAFNKASYFGMK 255
Db 184 MNGDSETCGTMTSGSISILACLAHNRRLKRGKYTEMIIVPSVHAFAEFAECERIK 243
Qy 256 IIVRVPFLKM-MEVDVRAHRRARISNNTAMLCSPQEPHGYIDPYPEAKLAVKYKTLHY 314
Db 244 VRKIPVDVPTFKVDLVKMAKAINKRCMLVGSAPNFPFGTVDDTEALIGQLGEYDIPVH 303
Qy 315 DACLGFLIYFMERAGYPLHPFDFRYKGYTISADTHKYGAPKSGSLVLYSDKKRYNY 374
Db 304 DACLGFLPFLEED---EIRYDFRPVSSISADSHKXGLAPKSSVLYRKKELJHN 359
Qy 375 QEFVVDMDMGITASPTIAGSRPGISAAACALMHGEGYEATQIITKTAFLKSEL 434
Db 360 QYFCDDMGGITASATMGSRAHNTALCWAALYHAQEGYANARKIVDTTRKIRNGL 419
Qy 435 ENIKGIFVFGNPNOLSLALGSRD-FDIYRLSNLMTAKGWNLNOLQPPSIHFCITLLHAR 493
Db 420 SNIKGIRKLGSPDVCISWNTNGVELYRPHNEMKEKHMQLNGIQFPAGHIMVTMHTH 479
Qy 494 KRAVIOFLKDIRSVTQIM--KNPKAKTGMGAITYAMAQTVDNRNVAELSSVFLDSLVS 551

Db 480 PGLAEAFVADCRAAVEFVKSHKPSSEDKTSEAAIYGLAQSIIPDRSLVHEFAHSYIDAVYA 539
Search completed: October 6, 2003, 13:52:00
Job time : 28 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 12:36:00 : Search time 50 Seconds
(without alignments)
1803.134 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLMLKAFEPYLEIL.....LYSDIVTQSGSQMGSPKPH 568

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues
Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24:	/SIDSL/gcgdata/geneseq/genescp-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2977	100.0	568	20	Human sphingosine-1-phos
2	2959	99.4	568	20	Human protein SEO
3	2952	99.2	580	22	Human protein SEO
4	2952	99.2	580	22	Human protein SEO
5	2553	85.8	568	20	Mouse sphingosine-1-phos
6	2498	83.9	488	20	Human altered sph
7	1344	45.1	545	22	Drosophila melanog
8	1344	45.1	545	22	Drosophila melanog
9	1344	45.1	545	22	Drosophila melanog

10	1008	33.9	542	20	AAV05828
11	1007.5	33.8	589	20	AAV05829
12	1007.5	33.8	589	22	AAV070706
13	949	31.9	589	22	AAV070849
14	514.5	17.3	384	22	AAV06568
15	355	11.9	76	20	AAV15212
16	275	9.2	133	21	AAV23455
17	261.5	8.8	466	23	AAV54627
18	258.5	8.7	125	21	AAV23456
19	258.5	8.7	466	19	AAV5165
20	234	7.9	467	23	AAV48689
21	233.5	7.8	496	23	AAO15137
22	233	7.8	500	23	AAO15139
23	232.5	7.8	464	23	ABBA9717
24	230.5	7.7	514	22	AAV6992
25	230	7.7	502	23	ABV9521
26	229	7.7	112	22	AAV80897
27	229	7.7	112	22	AAV83347
28	228.5	7.7	496	23	AAO15138
29	227	7.6	502	23	AAO15132
30	226	7.6	494	23	AAO15133
31	226	7.6	494	23	ABV91465
32	225	7.6	101	21	AAV23457
33	218.5	7.3	462	23	ABBA47826
34	211.5	7.1	494	23	AAO15136
35	211.5	7.1	494	23	ABV92352
36	209	7.0	502	23	AAO15140
37	207.5	7.0	494	21	AAV13764
38	207.5	7.0	507	21	AAV13765
39	203.5	6.8	464	21	AAV13765
40	202	6.8	500	23	AAO15134
41	202	6.8	500	23	ABV1694
42	198	6.7	493	23	AAO15135
43	198	6.7	493	23	ABV1695
44	181	6.1	609	22	ABV1670
45	180.5	6.1	1042	22	ABV1675

ALIGNMENTS

RESULT 1	
AAV05827	standard; Protein; 568 AA.
ID	AAV05827;
AC	AAV05827;
DT	02-AUG-1999 (first entry)
DE	Human sphingosine-1-phosphate lyase.
KW	Sphingosine-1-phosphate lyase; SFL; human; breast cancer;
KW	diagnosis; prognosis; therapy.
OS	Homo sapiens.
PN	W09916888-A2.
PD	08-APR-1999.
PF	29-SEP-1998; 98WO-US20365.
PR	29-SEP-1997; 97US-0939309.
PA	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
PI	Saba JD, Zhou J;
DR	WPT: 1999-263700/22.
PT	N-PSDB; AAX23567.
XX	Sphingosine-1-phosphate lyase, polynucleotides and modulators

PS Claim 9; Page 72-75; 96pp; English.

CC The present sequence represents human endogenous
CC sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the
CC cleavage of sphingosine-1-phosphate into inactive metabolites.
CC Sphingosine-1-phosphate is an endogenous tumour suppressor lipid
CC that potentially inhibits breast cancer cell growth and invasiveness,
CC while not affecting the growth of non-tumour cells. Mouse and
CC human SPL polynucleotides (see AAX2566-67) and polypeptides (see
CC AAY05826-29) are claimed. Methods are provided for preparing SPL
CC using transformed or transfected host cells. SPL polypeptides are
CC used in claimed methods for identifying agents that modulate SPL
CC activity. An SPL inhibitor will inhibit growth of cancer cells,
CC especially breast cancer cells. SPL inhibitors (polynucleotides
CC preventing expression of SPL genes, or antibodies against SPL) can
CC also be used to prevent the development and/or metastasis of
CC cancer, especially where the inhibitor is linked to an antitumour
CC or antileptrogen receptor antibody. Detection of alterations in an
CC endogenous SPL sequence, especially where the alteration is a
CC deletion of residues 334-433 of the 568 amino acid human SPL
CC sequence (see also AAY05830), can be used to diagnose cancer, and to
CC assess the prognosis for recovery.

XX Sequence 568 AA:

Query Match 100.0%; Score 2977; DB 20; Length 568;
Best Local Similarity 100.0%; Pred. No. 1.4e-281;
Matches 568; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLIWGYEYV 60
DB 1 MSTDLMLKAFPEYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLIWGYEYV 60
QY 61 FQESLMSRFRKKCFKLTTRKMPITGRKIDKLTKTDISKNNSEFLKVDKEYKALPSSG 120
DB 61 FQESLMSRFRKKCFKLTTRKMPITGRKIDKLTKTDISKNNSEFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
QY 181 LKRIEAEIVRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
DB 181 LKRIEAEIVRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
QY 241 AHAFAFKKASYSFGMKIVRPLTRKMEVDVRAAMRAISRNTAMLYCSTPPPHGVIDPVE 300
DB 241 AHAFAFKKASYSFGMKIVRPLTRKMEVDVRAAMRAISRNTAMLYCSTPPPHGVIDPVE 300
QY 301 VAKLAVKXKIPHLVDACLGFLIVMEKAGYPLEHPDFRWKGVTSISADTRKYGYPKG 360
DB 301 VAKLAVKXKIPHLVDACLGFLIVMEKAGYPLEHPDFRWKGVTSISADTRKYGYPKG 360
QY 361 SSVLYASDCKKRYNOFEVTDWOGGIYASPTIAGSPGGISAAACMAALHFGNGVEXT 420
DB 361 SSVLYASDCKKRYNOFEVTDWOGGIYASPTIAGSPGGISAAACMAALHFGNGVEXT 420
QY 421 KOIITKARFLKSELEIKIGIFVGNPOLSLIALGSDPDIYRLSNMTAKGNLNDLOPP 480
DB 421 KOIITKARFLKSELEIKIGIFVGNPOLSLIALGSDPDIYRLSNMTAKGNLNDLOPP 480
QY 481 PSIHFCITLLHARKRAVAIOFLKDIRESVTQIMKNPRAKTTGMAIYAMAQTVDRMVAE 540
DB 481 PSIHFCITLLHARKRAVAIOFLKDIRESVTQIMKNPRAKTTGMAIYAMAQTVDRMVAE 540
QY 541 LSSVFLDSLXTDTYVQSGOMNGSPKPH 568
DB 541 LSSVFLDSLXTDTYVQSGOMNGSPKPH 568

RESULT 2
AAY15211
ID AAY15211 standard; Protein; 568 AA.

XX AAY15211;
AC 26-OCT-1999 (first entry)
XX Sphingosine-1-phosphate lyase amino acid sequence.
DE Sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
KW G-protein coupled receptor; EDG-1; secondary messenger; cancer;
KW cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
KM stroke; apoptosis.
XX Homo sapiens.
OS Key Location/Qualifiers
FH Protein 1..568
FT /label= "Sphingosine-1-phosphate lyase"

XX WO9938983-A1.
XX 05-AUG-1999.
XX 24-DEC-1998; 98WO-EP08564.
XX 03-NOV-1998; 98GB-0024026.
XX 29-JAN-1998; 98EP-0300625.
XX (SMK) SMITHKLINE BEECHAM PLC.

PI Duckworth DM, Godden RJ, Testa TR;
XX WPI; 1999-479192/40.
XX N-PSDB; AA206342.

PT A new sphingosine-1-phosphate lyase useful for diagnosing and
PT treating cancers, cardiovascular disorders, thrombosis or
PT atherosclerosis
PS Claim 1; Page 23-24; 37pp; English.

CC This is the amino acid sequence of Sphingosine-1-phosphate lyase. The
CC lyase catalyses the cleavage of Sphingosine-1-phosphate to give a long
CC chain aldehyde and phosphoethanolamine.
CC The sequence has use as a method of treating cancers, cardiovascular
CC disorders, thrombosis, atherosclerosis and other conditions. This is due
CC to the action of Sphingosine-1-phosphate intracellularly as a secondary
CC messenger and extracellularly as a ligand for the G-protein coupled
CC receptor EDG-1.

XX Sequence 568 AA:

Query Match 99.4%; Score 2959; DB 20; Length 568;
Best Local Similarity 99.5%; Pred. No. 7.9e-280;
Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSTDLMLKAFPEYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLIWGYEYV 60
DB 1 MSTDLMLKAFPEYLEILEVYSTKAKNVNGHCTYEPWQLAWSVMTLLIWGYEYV 60
QY 61 FQESLMSRFRKKCFKLTTRKMPITGRKIDKLTKTDISKNNSEFLKVDKEYKALPSSG 120
DB 61 FQESLMSRFRKKCFKLTTRKMPITGRKIDKLTKTDISKNNSEFLKVDKEYKALPSSG 120
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
DB 121 LSSSAVLEKLEKSSMDAFWQEGRASGTYSGEKLTELLVYKAGDFAMSNPLHPDIFPG 180
QY 181 LKRIEAEIVRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
DB 181 LKRIEAEIVRIACSLFNGPDSGCVTSGTESILMACACRDLAEKGIKPEIYAPQS 240
QY 241 AHAFAFKKASYSFGMKIVRPLTRKMEVDVRAAMRAISRNTAMLYCSTPPPHGVIDPVE 300
DB 241 AHAFAFKKASYSFGMKIVRPLTRKMEVDVRAAMRAISRNTAMLYCSTPPPHGVIDPVE 300

Db 2A1 AHAFAFNKASVFGMKIVRPLTKMEVDVRAARRAISRTNTAMLCSTPQFPFGVIDPVE 300
 QY 301 VAKLAVKKYKIPLVHACLGFLIVEMERAGYPLEHPDFRVKGYTSSISADTHKGYAPRG 360
 Db 301 VAKLAVKKYKIPLVHACLGFLIVEMERAGYPLEHPDFRVKGYTSSISADTHKGYAPRG 360
 QY 361 SSVLVSDKRYRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 Db 361 SSVLVSDKRYRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 QY 421 KOIITARFLKSELENIGKIFVGNPQLSLALGSRDPIYRLSNLMTAKGNLQLOFP 480
 Db 421 KOIITARFLKSELENIGKIFVGNPQLSLALGSRDPIYRLSNLMTAKGNLQLOFP 480
 QY 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 Db 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 Db 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 3 AAM78461

ID AAM78461 standard; Protein: 568 AA.

AC AAM78461;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 1123.

KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.

OS Homo sapiens.

PN W0200157190-A2.

PD 09-AUG-2001.

PE 05-FEB-2001; 2001WO-US04098.

PR 03-FEB-2000; 2000US-0496914.

PR 27-APR-2000; 2000US-0560875.

PR 20-JUN-2000; 2000US-0598075.

PR 19-JUL-2000; 2000US-0620325.

PR 01-SEP-2000; 2000US-0654936.

PR 15-SEP-2000; 2000US-0663561.

PR 20-OCT-2000; 2000US-0693325.

PR 30-NOV-2000; 2000US-0728422.

DR WPI; 2001-476283/51.

DR N-PSDB; AAK51594.

PT Nucleic acids encoding polypeptides with cytokine-like activities,
 useful in diagnosis and gene therapy -

PS Claim 20; Page 3353-3354; 6221pp; English.

CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
 CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity relating to
 CC cytokine, cell proliferation or cell differentiation or which may induce
 CC production of other cytokines in other cell populations. The

CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
 CC peptide therapy. The polypeptides have various cytokine-like activities,
 CC e.g. stem cell growth factor activity, haematopoiesis regulating
 CC activity, tissue growth factor activity, immunomodulatory activity and
 CC activity/inhibit activity and may be useful in the diagnosis and/or
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
 CC inflammation.
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
 CC (AAM80020) are omitted as the relevant pages from the sequence listing
 CC were missing at the time of publication.

XX SQ Sequence 568 AA:

Query Match 99.4%; Score 2959; DB 22; Length 568;

Best Local Similarity 99.5%; Pred. No. 7.9e-280;

Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHGTRKFERWOLIAMSVVTLTIWQYEFV 60
 Db 1 MPSTDLMLKAFEPYLEILEVYSTAKNVNCHGTRKFERWOLIAMSVVTLTIWQYEFV 60
 QY 61 FQPELSMSRFRKKCKRTPKMBITIGRTODKLNKTKDTSKMSFLKVDKVEYKALPSQG 120
 Db 61 FQPELSMSRFRKKCKRTPKMBITIGRTODKLNKTKDTSKMSFLKVDKVEYKALPSQG 120
 QY 121 LSSSAVLEKLEKYEYSSMDAFWQEGRASGTYVSGEEKLTLLVAYAGDFAMSNLHPDIFPG 180
 Db 121 LSSSAVLEKLEKYEYSSMDAFWQEGRASGTYVSGEEKLTLLVAYAGDFAMSNLHPDIFPG 180
 QY 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACBDLAFENKIKTPEIYAPOS 240
 Db 181 LKRIAEIVRIACSLFNGGPDSCGCVTSGGTESIIMACKACBDLAFENKIKTPEIYAPOS 240
 QY 241 AHAFAFNKASVFGMKIVRPLTKMEVDVRAARRAISRTNTAMLCSTPQFPFGVIDPVE 300
 Db 241 AHAFAFNKASVFGMKIVRPLTKMEVDVRAARRAISRTNTAMLCSTPQFPFGVIDPVE 300
 QY 301 VAKLAVKKYKIPLVHACLGFLIVEMERAGYPLEHPDFRVKGYTSSISADTHKGYAPRG 360
 Db 301 VAKLAVKKYKIPLVHACLGFLIVEMERAGYPLEHPDFRVKGYTSSISADTHKGYAPRG 360
 QY 361 SSVLVSDKRYRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 Db 361 SSVLVSDKRYRNYQFVDTDMOGGIYASPTIAGSRPGISAAACMAALMHFGENGVEAT 420
 QY 421 KOIITARFLKSELENIGKIFVGNPQLSLALGSRDPIYRLSNLMTAKGNLQLOFP 480
 Db 421 KOIITARFLKSELENIGKIFVGNPQLSLALGSRDPIYRLSNLMTAKGNLQLOFP 480
 QY 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 Db 481 PSIHFCITLLHARKKRVAIQFLKDIRESVYQIMKNPKAKTTGGAITYAMAQTTVDNRMYAE 540
 QY 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568
 Db 541 LSSVFLDSLSTDTVTQGSQMGNSPKPH 568

RESULT 4 AAM79445

ID AAM79445 standard; Protein: 580 AA.

AC AAM79445;

DT 06-NOV-2001 (first entry)

DE Human protein SEQ ID NO 3091.

KM Human: cytokine; cell proliferation; cell differentiation; gene therapy;
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;
 KM nervous system disorder; arthritis; inflammation.

OS Homo sapiens.
PN WO200157190-A2.
XX 09-AUG-2001.
XX 05-FEB-2001; 2001MO-US04098.
XX 03-FEB-2000; 2000US-0496914.
XX 27-APR-2000; 2000US-0560875.
XX 20-JUN-2000; 2000US-0598075.
XX 19-JUL-2000; 2000US-0620325.
XX 01-SEP-2000; 2000US-0654936.
XX 15-SEP-2000; 2000US-0663561.
XX 20-OCT-2000; 2000US-0693325.
XX 30-NOV-2000; 2000US-0728422.
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Zhang J, Ren F, Chen R, Wang ZM;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
DR N-PSDB; AAK52578.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 249; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAK78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAK60020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 580 AA:
SQ
Query Match 99.2%; Score 2952; DB 22; Length 580;
Best Local Similarity 99.3%; Pred. No. 3.9e-279;
Matches 364; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 MSTDDLMLKAFEPYLEILEVYSTKAKNVNGHCTKYEPMQILAMSVVMTLLVMGVEFY 60
DB 13 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTKYEPMQILAMSVVMTLLVMGVEFY 72
QY 61 FQESLMSRRKKCKEFLTRKMPILIGRKIDOKLTKTRDISKNSFLKVDKEYKALPSSQ 120
DB 73 FQESLMSRRKKCKEFLTRKMPILIGRKIDOKLTKTRDISKNSFLKVDKEYKALPSSQ 132
QY 121 LSSSAVLEKLEKSSMDAFWQEGRASGYTSSGEKTELLVKKYGDFAVSNPLHPDIFPG 180
DB 133 LSSSAVLEKLEKSSMDAFWQEGRASGYTSSGEKTELLVKKYGDFAVSNPLHPDIFPG 192
QY 181 LKRIEAIYRIACSLFNGSGCGVTSGETESIILAKACRDLAFKEGKTPEIYAPQS 240
DB 193 LKRIEAIYRIACSLFNGSGCGVTSGETESIILAKACRDLAFKEGKTPEIYAPQS 252
QY 241 AAAAFKKAASYFGMKIVRPLTKMMEVDVRAVRRAISRTAMLVCSPTOPPHGVIDPVE 300
DB 253 AAAAFKKAASYFGMKIVRPLTKMMEVDVRAVRRAISRTAMLVCSPTOPPHGVIDPVE 312
QY 301 VAKLAVKXKIPILHVDACLGGLIVFMEKAGYPLEHFPDRVKGVTISADTRKYYGAPKG 360

DB 313 VAKLAVKXKIPILHVDACLGGLIVFMEKAGYPLEHFPDRVKGVTISADTRKYYGAPKG 372
QY 361 SSLVYSDKKRYNPFVDPMOGGITYASPTIAGSRPGISACMAALMHFGENGYEAT 420
DB 373 SSLVYSDKKRYNPFVDPMOGGITYASPTIAGSRPGISACMAALMHFGENGYEAT 432
QY 421 KQIITARFLKSELENIKGIFVFGNPQLSIALGSRDFDIYRLSNLMTAKGNLNOLOFP 480
DB 433 KQIITARFLKSELENIKGIFVFGNPQLSIALGSRDFDIYRLSNLMTAKGNLNOLOFP 492
QY 481 PSTHFCITLHARKRAVIOFLKDIRESVTOIMNPKAKTGMCAIYAMAOTVDRNVAAE 540
DB 493 PSTHFCITLHARKRAVIOFLKDIRESVTOIMNPKAKTGMCAIYAMAOTVDRNVAAE 552
QY 541 LSSVFLDSLXTDTVTYQSGMNSPKPH 568
DB 553 LSSVFLDSLXTDTVTYQSGMNSPKPH 580
RESULT 5
AAV05826
ID AAV05826 standard; Protein; 568 AA.
XX
XX AAV05826;
XX
XX 02-AUG-1999 (first entry)
XX
XX Mouse sphingosine-1-phosphate lyase.
XX
XX Sphingosine-1-phosphate lyase; SPL; mouse; breast cancer;
XX diagnosis; prognosis; therapy.
XX
XX Mus musculus.
XX
XX W09916888-A2.
XX
XX 08-APR-1999.
XX
XX 29-SEP-1998; 98WO-US20365.
XX
XX 29-SEP-1997; 97US-0939309.
XX
XX (CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.
XX
XX Saba JD, Zhou J;
XX
XX WPI: 1999-263700/22.
XX
XX N-PSDB; AAX25566.
XX
XX Sphingosine-1-phosphate lyase, polynucleotides and modulators
XX Claim 9; Page 64-67; 96pp; English.
XX
XX The present sequence represents murine endogenous
XX sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the
XX cleavage of sphingosine-1-phosphate into inactive metabolites.
XX Sphingosine-1-phosphate is an endogenous tumour suppressor lipid
XX that potentially inhibits breast cancer cell growth and invasiveness,
XX while not affecting the growth of non-tumour cells. Mouse and
XX human SPL polynucleotides (see AAX25566-67) and polypeptides (see
XX AAV05826-29) are claimed. Methods are provided for preparing SPL
XX using transformed or transfected host cells. SPL polypeptides
XX used in claimed methods for identifying agents that modulate SPL
XX activity. An SPL inhibitor for identifying agents that modulate SPL
XX especially breast cancer cells. SPL inhibitors (polynucleotides
XX preventing expression of SPL genes, or antibodies against SPL) can
XX also be used to prevent the development and/or metastasis of
XX cancer, especially where the inhibitor is linked to an antitumour
XX or antioestrogen receptor antibody. Detection of alterations in an
XX endogenous SPL sequence can be used to diagnose cancer, and to
XX assess the prognosis for recovery.

Seq	Sequence	568 AA;
Query Match	85.8%; Score 2553; DB 20; Length 568;	
Best Local Similarity	84.1%; Pred. No. 3,8e-240;	
Matches	477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;	
QY	1 MPSTDLMLKAFEPPELLELEYSTAKNTVNGCHTKRYEPMQLIAMSVVWTLIIWGYEFV	60
DB	1 MPGDLDLKLKFEPELLELESYSTAKNTVNGCYCTKYPEMQLIAMSVCITLLIIVWYELI	60
QY	61 FQPSLWSPFKKCKKTLRKMPITIGRKIDKINKTKDIDISKMSFLYDKXEYKALPSQG	120
DB	61 FQPSLWSPFKKCKKTLRKMPETIGRKIDKINKTKDIDISKMSFLYDKXEYKALPSQG	120
QY	121 LSSAVLESLKLEYSMDAFWQEGRASGVTVYSGSEKLTETLLYKAYDDFAWNPDLHPDIFG	180
DB	121 MGTAVLESLKLEYSMDQSGKSGAVYNEPKLTETLLYQAYGEFTMSNPLHDPDIFG	180
QY	181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESSIMACKACHDLAEFGIKTPETIYAPDS	240
DB	181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESSIMACKACHDLAEFGIKTPETIYAPDS	240
QY	241 AHAANKASVFGMKIVIVPPLTKMDEVYRAIRARLISRTAALVLCSTQEPFGVYDVPVE	300
DB	241 AHAANKASVFGMKIVIVPPLTKMDEVYRAIRARLISRTAALVLCSTQEPFGVYDVPVE	300
QY	301 VAKLAVKKIKPLHVDACLGGLIYEMEKAGYPLEHPDFRYGVTSISADTHKYGAPKG	360
DB	301 VAKLAVKKIKPLHVDACLGGLIYEMEKAGYPLEHPDFRYGVTSISADTHKYGAPKG	360
QY	361 SSVLVYSDKKKXRNQVFEVDTDWQGGIYASPTIAGSRPGGISAAACMAALMHFEGENCYVEAT	420
DB	361 SSVLVYSDKKKXRNQVFEVDTDWQGGIYASPTIAGSRPGGISAAACMAALMHFEGENCYVEAT	420
QY	421 KOIITAFAPLSELENIGIYFEGNPQSLIALSGRSDIYRLSNLMTAKGNLNOLEP	480
DB	421 KOIITAFAPLSELENIGIYFEGNPQSLIALSGRSDIYRLSNLMTAKGNLNOLEP	480
QY	481 PSIHFCITLLHARRKKEVAIOFLKDIDRESYTOIMKNPKAKTGTGATYAMAQTVDRNMVAE	540
DB	481 PSIHFCITLLHARRKKEVAIOFLKDIDRESYTOIMKNPKAKTGTGATYAMAQTVDRNMVAE	540
QY	541 LSSVFLDSLYSTDTVTQSGOMNGSKRP 567	
DB	541 LSSVFLDSLYSTDTVTQSGOMNGSKRP 567	
RESULT 6		
AAV05830		
ID	AAV05830 standard; Protein; 488 AA.	
AC	AAV05830;	
XX		
DT	02-AUG-1999 (first entry)	
XX		
DE	Human altered sphingosine-1-phosphate lyase.	
XX		
KW	Sphingosine-1-phosphate lyase; SRP; human; breast cancer; diagnosis; prognosis; therapy; deletion.	
XX		
OS	Homo sapiens.	
PN	W09916868-A2.	
XX		
PD	08-APR-1999.	
XX		
PF	29-SEP-1998; 98WO-US20365.	
XX		
PR	29-SEP-1997; 97US-0939309.	
XX		
PA	(CHIL-) CHILDREN'S HOSPITAL OAKLAND RES INST.	
XX		
PI	Saba JD, Zhou J;	

XX WP1. 1999-263700/22.
 DR N-PSDB: AAX23570.
 XX
 XX Sphingosine-1-phosphate lyase, polynucleotides and modulators
 XX Example 3; Page 94-96; 96pp: English.
 XX
 CC The present sequence represents sphingosine-1-phosphate lyase (SPL),
 CC as predicted from cDNA (see AAX25570) obtained by amplification of
 CC human glioblastoma multiforme RNA. The polypeptide sequence lacks
 CC amino acids 354-433 of SPL (see AY05827) predicted from a clone
 CC obtained from fibroblast cells. Sphingosine-1-phosphate is an
 CC endogenous tumour suppressor lipid that potentially inhibits breast
 CC cancer cell growth and invasiveness, while not affecting the growth
 CC of non-tumour cells. Detection of alterations in an endogenous SPL
 CC sequence, especially where the alteration is a deletion of residues
 CC 354-433 of the 568 amino acid human SPL sequence, can be used to
 CC diagnose cancer, and to assess the prognosis for recovery. Mouse and
 CC human SPL polynucleotides (see AAX2566-67) and polypeptides (see
 CC AAY05826-29) are claimed. The polypeptides are used in claimed methods
 CC for identifying agents that modulate SPL activity. SPL inhibitors
 CC will inhibit growth of cancer cells, especially breast cancer cells.
 CC They can also be used to prevent the development and/or metastasis
 CC of cancer, especially where the inhibitor is linked to an anti-tumour
 CC or anti-oestrogen receptor antibody.
 CC
 XX
 XX Sequence 488 AA:
 SQ
 Query Match 83.9%; Score 2498; DB 20: Length 488;
 Best Local Similarity 85.9%; Pred. No. 7.1e-235;
 Matches 488; Conservative 0; Mismatches 0; Indels 80; Gaps 1

QY	1	MPSTDLMLKAEPYLEILEVYSTKAKNVNGCHCTYPEPMOLIANVYVWTLIIWNGYEFV	60
DB	1	MPSTDLMLKAEPYLEILEVYSTKAKNVNGCHCTYPEPMOLIANVYVWTLIIWNGYEFV	60
QY	61	FQPELSMRFKKKCKRLTRKMPITIRKTIQDKLNKTKKDDISKMSFLXKDXEVKALPSQG	120
DB	61	FQPELSMRFKKKCKRLTRKMPITIRKTIQDKLNKTKKDDISKMSFLXKDXEVKALPSQG	120
QY	121	ISSAVLEKLKLEYSEMDAFWQEGRASGVYSGEEKITELLYNAYGDFAMSNPLHDPFPG	180
DB	121	ISSAVLEKLKLEYSEMDAFWQEGRASGVYSGEEKITELLYNAYGDFAMSNPLHDPFPG	180
QY	161	LKRIAEIVRIACSLFNGPDSGCVTSGGTESILMACACADLAPENGKIKTPEIYAPQS	240
DB	161	LKRIAEIVRIACSLFNGPDSGCVTSGGTESILMACACADLAPENGKIKTPEIYAPQS	240
QY	241	AHAAFNKASVYGMKIVRPLTKMMEVYRARRAIRISRTALVCSFOFPGVADPVE	300
DB	241	AHAAFNKASVYGMKIVRPLTKMMEVYRARRAIRISRTALVCSFOFPGVADPVE	300
QY	301	VAKLAVKKKIPLVNACLGGELIVIMERAGYPLEHPDFRVKGVYSISADTHKYGAPRG	360
DB	301	VAKLAVKKKIPLVNACLGGELIVIMERAGYPLEHPDFRVKGVYSISADTHKYGAPRG	360
QY	361	SSLVLYSDKKIRNYQFVVDTMQGGITVSPITAGSRPGGISAACMAALMHFGENGVEAT	420
DB	361	SSLVLYSDKKIRNYQFVVDTMQGGITVSPITAGSRPGGISAACMAALMHFGENGVEAT	420
QY	421	KQIKTARFLKSELENIGIFVFGNPOLSLIALGSRDDIYRLSNLMTAKGNLNLQLOFP	480
DB	421	KQIKTARFLKSELENIGIFVFGNPOLSLIALGSRDDIYRLSNLMTAKGNLNLQLOFP	480
QY	481	PSIHFCITLHARKRVAIQFLKDINESYTOIMKNKPAKTTGCAIYAAQOTVDRNVAE	540
DB	481	PSIHFCITLHARKRVAIQFLKDINESYTOIMKNKPAKTTGCAIYAAQOTVDRNVAE	540
QY	541	LSVFLDSLSTDTYTOGSONMGSKRP 568	
DB	541	LSVFLDSLSTDTYTOGSONMGSKRP 568	
QY	461	LSVFLDSLSTDTYTOGSONMGSKRP 488	
DB	461	LSVFLDSLSTDTYTOGSONMGSKRP 488	

```
RESULT 7
ID ABB64094 standard; Protein; 545 AA.
AC ABB64094.
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 19074.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI: 2001-656860/75.
XX N-PSDB; ABL08197.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 19074; 21pp + Sequence Listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABBS7737-ABBS72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 545 AA;
XX
Query Match 45.1%; Score 1344; DB 22; Length 545;
Best Local Similarity 49.0%; Pred. No. 5.5e-122;
Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4;
OY 38 EPMQIAMSVMVTLIVMGVEEVEFQPELSMRKKKCFLTRKPIIGRKIDKLNKTRD 97
DB 25 EPMQVATVATVATVGLGVWLMVYICODENLYIGRKQRFPAKKIPAVRQVDELAKKAN 84
OY 98 DISKNNSEFLKVDKEYKALPSSGLSSANVLEKIKESMDAP-WQGRASGVTVSSEEL 156
DB 85 DETETLKSSNAHLTYSETLPEKGLSKKEELRLVDEHLKTHGHWNRDGRVSGAIVGYKPD 144
OY 157 TELLVKAYGDFAMSNPLHDPFGPLRKIEATVIRICSLFNGGPPDSCGCGVSGGTESILM 216
DB 145 VELIVEVIGKASTINLHADLPFGVCKMEAEVVRMACNLFHGSASCGTMTTGGTESIVM 204
OY 217 ACKACRDIAFE-KGKITPEIIVAPQSAHAFAFNKASFGKAIYRVP-L-TMMEDVVRAMR 274
DB 205 AMKAVRDFARREYKGIIRPIVYKTYHAHAFDGGCFNFHIVHSVDVDEPTVEVDIKKFR 264
OY 275 AISRNTAMLVGSTPOFPHGVDPVPEVAKLAVKIKIPILHVDACLGGELIVMEKAGPYLE 334
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DB 265 AINRNTILLVGSAPNPFYGFIDIDEAIAAGVXYDIPVHVDACLSFVALVYNAGYKL- 323
OY 335 HPFDFRVKGVSTISADPHKRYGAPKGSLLVYSDKRYRNQFVDDMOGGIASPPIAG 394
DB 324 RPFDFEVKGVTSISADPHKRYGAPKGSLLVYSDKRYKHQFTVTTDMRGVGSPTVNG 383
OY 395 SRPGISAACMAALMHGNGEYVEATKQIIRKARPLKSELENKIGFVGNPOLSLALG 454
DB 384 SRAGGIIAACWATMMSFGVDGYELATRKRIYDARFYERGVROIDGFIIGKPAVSIALG 443
OY 445 SRPFDIYRLSNLMTAKGWNINOLQPPSPHFCITLLHARKRAVIOFLKDIRESVTOIMKN 514
DB 444 SNVFEDIFRLSDSLCKLGWNLNALQFPSSVILYSDKRYKHQFTVTTDMRGVGSPTVNG 503
OY 515 PRAKTTMGATVMAQTVDNRNVAELSSVFLDSLST 552
DB 504 PGOPVYGKMAIYGAOSIPDRSVIGEVTRFLFLSHMYT 541
```

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RESULT 8
ID ABB64099 standard; protein; 545 AA.
AC ABB64099.
DT 26-MAR-2002 (first entry)
XX Drosophila melanogaster polypeptide SEQ ID NO 19089.
XX
XX Drosophila; developmental biology; cell signalling; insecticide;
XX pharmaceutical.
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PMD, Myers EW;
XX
XX MPI: 2001-656860/75.
XX N-PSDB; ABL08202.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Disclosure; SEQ ID NO 19089; 21pp + Sequence Listing; English.
XX
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABBS7737-ABBS72072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX
XX Sequence 545 AA;
XX
Query Match 45.1%; Score 1344; DB 22; Length 545;
Best Local Similarity 49.0%; Pred. No. 5.5e-122;
```

Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4;	
OY	38 EPMOLIMSVYVTLIIWVGFEVFPQESIMSRFKKCKLRLKMPITIGRKIODLKNRKD 97
Db	25 EPMOVATITATTVTLGGVWLMVTVICODENLITRGKROFFKAKKIPAVAROVETELAKKN 84
OY	98 DISKMSFLKYDKEYVALPSQGLSSSAVLEKLEKYESMDAF-WOEGRASGTVYSGEKL 156
Db	85 DFEIEIKSNMHLTYSETLPEKGLSKEIILRLVDEHLKTHGYNMRDGVSAVYGYKRD 144
OY	157 TELLVKAYGDRAMNPLHPDIFPGLRKIEAIVRIACSLFNGGPDSCGCVTSGTESTILM 216
Db	145 VELTVEYVGKASYNPLHADLFPVCCKMEAEVVRMACLFFHNSASCSCTMTTGGTESTIV 204
OY	217 ACKACRDLAFE-KGIKRPEIYAPOSANAHAFKKAASYFGMKIVRYPL-TKMEDEVYRAMR 274
Db	205 AMKAYRDPFAREYKGIITRNIVYPTVHAAPFGKGOYFIHRSVDVDEYEVDIKKFKR 264
OY	275 AISHNTAMLCSTQPFPHGVIDPYPEVAKLVKTKIPLHVDACLGFLIVEMERAGYPLE 334
Db	265 AINNTITLLVGSANFNPGTIDIDIEAIALGVKVDIPVHDACLSGFVALVRNAGYKL- 323
OY	335 HPFDFRKYGVTSISADTHKKYGYAPKGSLLVYSOKTKRNYOFFVDTMOGGIYASPTIAG 394
Db	324 RPFDFEYKGVTSISADTHKKYGFAPKGSVLIYSKRYKDHQFTVTTDMPGCVGSPYVNG 383
OY	395 SRPGISAAACMAALMHFENGUYVATKOIITARFLKSELNIGIIPFGNPOSLIATLG 454
Db	384 SRAGITACWATMMSRGYDGLATKRIYDTARIIEGVADIDGIFLFGAPATSVIALG 443
OY	455 SRDEDIYRLNMLMTAKGNLNLQLOFPSPSIHFCITLLHARKKVAIOFLKDIRESTYQIMKN 514
Db	444 SNVDFIRLSDSLCKLGNLNLALQFPGSIHLCTVDMHTQPCVADKFIADVASCRAELMKD 503
OY	515 PKATTGMAIYYAQAOTTVDRNMVAELSSVFLDSLST 552
Db	504 PGDPVVGKMALYGMAGOSIPDRSVIGEVYRLFLHSMYYT 541
RESULT 9	
AAE03543	
ID	AAE03543 standard; Protein: 545 AA.
XX	AAE03543;
AC	
XX	
DT	03-AUG-2001 (first entry)
XX	
DE	Drosophila melanogaster sphingosine phosphate lyase (SPL) protein.
XX	
KW	Fruit fly; sphingosine phosphate lyase; SPL; metazoan; insect;
KW	worm; pesticidal agent; therapeutic; pesticide; drug target.
XX	
OS	Drosophila melanogaster.
XX	
FH	Key
FT	Location/Qualifiers
FT	300..316
FT	/label-Transmembrane_domain
FT	192..306
FT	/note-"Pyridoxal dependent decarboxylase conserved domain"
FT	133..431
FT	/note-"PLP dependent enzyme domain"
FT	138..522
FT	/note-"Conserved domain of DcGT, DncJ, Eryc1 and Strs family"
FT	
XX	
PN	WO200142479-A2.
XX	
PD	14-JUN-2001.
XX	
PE	07-DEC-2000; 2000WO-US33320.
XX	
PR	08-DEC-1999; 99US-0169610.

PR	28-DEC-1999; 99US-0173228.
PR	28-DEC-1999; 99US-0173349.
XX	
PA	(GENO-) GENOPTERA LLC.
XX	
PI	Ebens AJ, Keegan KP, Stout TJ;
XX	
DR	WPI; 2001-381698/40.
DR	N-PSDB; AAD06842.
XX	
PT	Nucleic acid molecules encoding proteins that are useful for
PT	genetically modifying metazoan invertebrate organisms such as insects
PR	and worms, or cultured cells, resulting in expression of proteins -
XX	
PS	Claim 22; Page 57-58; 58pp; English.
XX	
CC	The invention relates to Drosophila melanogaster hellicase protein,
CC	phosphatidylinositol transfer protein (PITP), sphingosine phosphate lyase
CC	(SPL) protein and their corresponding nucleic acid molecules. These
CC	nucleic acids and proteins are useful for genetically modifying the
CC	metazoan invertebrate organisms such as insects and worms, resulting in
CC	expression or mis-expression of the encoded proteins. The genetically
CC	modified organisms or cells are used in screening assays to identify
CC	candidate compounds which are potential pesticide agents or therapeutics
CC	that interact with subject proteins. The invention also relates to method
CC	for studying the biological activity of subject proteins and identifying
CC	compounds that have utility as pesticides. The nucleic acids are useful
CC	for generating mutant phenotypes in animal models or in living cells that
CC	is used for studying the regulation of proteins and use of proteins as
CC	pesticides and drug targets. The present sequence is Drosophila
CC	melanogaster sphingosine phosphate lyase (SPL) protein.
XX	
SO	Sequence 545 AA;
Query Match 45.1%; Score 1344; DB 22; Length 545;	
Best Local Similarity 49.0%; Pred. No. 5.5e-122;	
Matches 254; Conservative 100; Mismatches 160; Indels 4; Gaps 4;	
OY	38 EPMOLIMSVYVTLIIWVGFEVFPQESIMSRFKKCKLRLKMPITIGRKIODLKNRKD 97
Db	25 EPMOVATITATTVTLGGVWLMVTVICODENLITRGKROFFKAKKIPAVAROVETELAKKN 84
OY	98 DISKMSFLKYDKEYVALPSQGLSSSAVLEKLEKYESMDAF-WOEGRASGTVYSGEKL 156
Db	85 DFEIEIKSNMHLTYSETLPEKGLSKEIILRLVDEHLKTHGYNMRDGVSAVYGYKRD 144
OY	157 TELLVKAYGDRAMNPLHPDIFPGLRKIEAIVRIACSLFNGGPDSCGCVTSGTESTILM 216
Db	145 VELTVEYVGKASYNPLHADLFPVCCKMEAEVVRMACLFFHNSASCSCTMTTGGTESTIV 204
OY	217 ACKACRDLAFE-KGIKRPEIYAPOSANAHAFKKAASYFGMKIVRYPL-TKMEDEVYRAMR 274
Db	205 AMKAYRDPFAREYKGIITRNIVYPTVHAAPFGKGOYFIHRSVDVDEYEVDIKKFKR 264
OY	275 AISHNTAMLCSTQPFPHGVIDPYPEVAKLVKTKIPLHVDACLGFLIVEMERAGYPLE 334
Db	265 AINNTITLLVGSANFNPGTIDIDIEAIALGVKVDIPVHDACLSGFVALVRNAGYKL- 323
OY	335 HPFDFRKYGVTSISADTHKKYGYAPKGSLLVYSOKTKRNYOFFVDTMOGGIYASPTIAG 394
Db	324 RPFDFEYKGVTSISADTHKKYGFAPKGSVLIYSKRYKDHQFTVTTDMPGCVGSPYVNG 383
OY	395 SRPGISAAACMAALMHFENGUYVATKOIITARFLKSELNIGIIPFGNPOSLIATLG 454
Db	384 SRAGITACWATMMSRGYDGLATKRIYDTARIIEGVADIDGIFLFGAPATSVIALG 443
OY	455 SRDEDIYRLNMLMTAKGNLNLQLOFPSPSIHFCITLLHARKKVAIOFLKDIRESTYQIMKN 514
Db	444 SNVDFIRLSDSLCKLGNLNLALQFPGSIHLCTVDMHTQPCVADKFIADVASCRAELMKD 503
OY	515 PKATTGMAIYYAQAOTTVDRNMVAELSSVFLDSLST 552
Db	504 PGDPVVGKMALYGMAGOSIPDRSVIGEVYRLFLHSMYYT 541

[illegible]

QY	256	IVRVAVLITKM-MEVDVPRAMRAAISRNAMVCSPPOPPHGVIDPVPYAKLAVKYPKPLHY	314
Db	244	VKRTIVDPVTEFVVDVLKMKAAIAINKRCMLVGSAPNPFEGTVDDIEAIGGLGLETDLFVHV	303
QY	315	DACLGGLFLVFEKAGPYLHEHFEDEFVKCVTSISADTHKYGYPARKSSSLVYSDKKYRNY	374
Db	304	DACLGGLFLFLFEED---EIRYDFEVPVSSISADSHKYGGLAPKSSSVLYLNKKELHN	359
QY	375	QEFVDTDMOGGIYASPTIAGSRPGGISAAQMAALMHFGENGVEYEAATKQITKARFLKSEL	434
Db	360	QYFCADMOGGIYASATMEGSRAGNIAICMAAMLETHAEGYANARKIYDTRKIRNGL	419
QY	435	ENIKIIFVFGNQSLIALGSRD-PIYELSLNMTKGGNNLOJRPSPSIHFCITLLHAR	493
Db	420	SNIKGIRKLOGPSDVCVTSWTTNDGVELLYRHHNMEKKEHQLGNLGPAGHVHIVTNKHTH	479
QY	494	KRAVLOFLKDIESYTOIWM-KNPKAKTGMCAIYVMAOTTVDRNNVAELSSVFLDSLVS	551
Db	460	PGLAFAFVADCAANAEVFKSHKRPSEDSKTSSEAIYVLGASIPDRSLVHEPASHYIDAVYA	539
RESULT 11			
AAV05829			
ID	AAV05829	standard; Protein; 589 AA.	
XX	AAV05829;		
AC	AAV05829;		
XX			
DT	02-AUG-1999	(first entry)	
XX			
DE	Yeast sphingosine-1-phosphate lyase.		
XX			
KM	Sphingosine-1-phosphate lyase; SPL; breast cancer; diagnosis;		
KW	prognosis; therapy; yeast.		
XX			
OS	Saccharomyces cerevisiae.		
XX			
PN	W09916888-A2.		
PD	08-APR-1999.		
XX			
PF	29-SEP-1998;	98WO-US20365.	
XX			
PR	29-SEP-1997;	97US-O939309.	
XX			
PA	(CHIL-) CHILDBREN'S HOSPITAL OAKLAND RES INST.		
XX			
PI	Saba JD, Zhou J;		
XX			
DR	WPI; 1999-263700/22.		
DR	N-PSDB; AAX25569.		
XX			
PT	Sphingosine-1-phosphate lyase, polynucleotides and modulators		
XX			
PS	Claim 11; Page 87-90; 96pp; English.		
XX			
CC	The present sequence represents Saccharomyces cerevisiae endogenous sphingosine-1-phosphate lyase (SPL), an enzyme that catalyses the cleavage of sphingosine-1-phosphate into inactive metabolites. Human sphingosine-1-phosphate is an endogenous tumour suppressor lipid that potentially inhibits breast cancer cell growth and invasiveness, while not affecting the growth of non-tumour cells. Yeast SPL is used in a claimed method for identifying agents that modulate SPL activity. SPL inhibitors will inhibit growth of cancer cells, especially breast cancer cells. SPL inhibitors, including polynucleotides preventing expression of SPL genes, or antibodies against SPL, can also be used to prevent the development and/or metastasis of cancer, especially where the inhibitor is linked to an antitumour or antioestrogen receptor antibody. Detection of alterations in an endogenous SPL sequence can be used to diagnose cancer, and to assess the prognosis for recovery.		
XX	Sequence	589 AA;	

PN W0200102550-A2.
XX 11-JAN-2001.
XX 03-JUL-2000; 2000MO-BE00077.
XX 01-JUL-1999; 99EP-0870141.
XX (JANC) JANSEN PHARM NV.
XX Contreras RH, De Backer MD, Luyten WHML, Malcorps IKL;
PI Nelissen BJM, Reekmans RJ;
XX WPI: 2001-367042/38.
DR N-PSDB; AAH2985.
XX
XX Yeast and fungal nucleic acids encoding proteins involved in a pathway
PT leading to programmed cell death, useful for treating proliferative
PT disorders, yeast and fungal infections, or for preventing apoptosis in
PT certain diseases -
XX
XX Claim 24: Fig 2; 218pp; English.
XX
XX The present invention provides the protein and coding sequences of a
CC number of apoptosis associated proteins from the yeast *Saccharomyces*
CC cerevisiae and the fungus *Candida albicans*. These can be used to identify
CC treatments for fungal and yeast infections, for proliferative diseases
CC and for apoptosis related diseases such as autoimmune diseases, ischaemia
CC and neurodegeneration. The present sequence is one of the *C. albicans*
CC proteins of the invention.
XX
SQ Sequence 589 AA:

Query Match 31.9%; Score 949; DB 22; Length 589;
Best Local Similarity 37.0%; Pred. No. 2,6e-83;
Matches 217; Conservative 107; Mismatches 202; Indels 60; Gaps 18;

OY 9 LKAPRYLEI---LEVSTKAKNYVNGH-CTKPYMOLIANVWTL-----IWGYE 58
DB 18 LTKAKIYQILKILFATYCAQSGFNGSVCLARD---IFGVYVYTLKLYRYLRGYG 74
OY 59 FVFEQESLW---SREKKKFKLTKRMPILIGRKIDDKINKTKMNSFLKVDKEYK 114
DB 75 IYDSIRRLIYVSVSSQIFSLPRISKIDKELATGKVEELMKN-----DPQLQ 128
OY 115 --ALPSSGLSSAV--LEKLEKXSSMDAFMOEGRASGVYSGEKLTELKAYGDPAM 169
DB 129 FPELEGGIDADNVSLLELDKLNKHS--WINGRVSAVYHGENLTLGVEAYKKYSV 186
OY 170 SNPLHDPLEPGRLKTEARIVRIACSLFNGSGCCVTSCTGTESTIMACKACROLAFE-K 228
DB 187 ANQLHPDVPFGVRKMEAEVHVHVDIFNAPSDCGSGTSGTESLLGLSAREYKKYR 246
OY 229 GIKTPEIYAPSAHAFAFKKASYFGMKIVRPLTKM-NEVDVRRARRAISRTATLVCS 287
DB 247 GITEEVYLAPTYIHGIEKACEYFGMKLHKVDLPVTQVDYKKERLINSTVILCSA 306
OY 288 POFHGVIDPVEVAKLAVKKYKIPLVHVDACLGGLIVMEKA-----GYPLEHDFRV 341
DB 307 PNYPGIIDIESTLKVAVKYNIPLVHVDACLSFVSLFKSKVHGDKRLP---FDRRL 363
OY 342 KGVTSISADTKHYGAPRGSSLVYSDKKRYNOFVDTMOGGIYASPTIAGSRPGIS 401
DB 364 PGVYSISCDTHKYGAPRGSSITIMRSPKLRCOYIYASDWTGMYGSPTLGSRPALV 423
OY 402 AACAAALHFGENGVEATKOIITKAPRLAKSELEN---IKGIFVGNPQLSLIL---- 453
DB 424 VGCATLNLNKGKGTCTKCYDIIVSASMKYKRAIEFDPLSKHLQITGPISVIFQLAP 483
OY 454 -GSRDEDIYRLSNLTAKGMLNLOQPPSIHFCITLLHARKKVALIQLKDIRESVTIM 512
DB 484 OOSGNLSIYEISDLTKKGWHFATLQNSALHFAFRTLV--PVVDELIADLVETKNAV 541

OY 513 -----KNPKAKTNG-MGAIYAMQTTVDKMMVAELSSVFIDSLY 550
DB 542 AIAEHKKNGVTKAPGDTALYGIAGSVHTAGLADRLIYAFIDTLY 587

RESULT 14
ID AAB96568 standard; Protein; 384 AA.
XX AAB96568;
AC AAB96568;
XX 29-OCT-2001 (first entry)
DE Putative P. abyssal glutamate decarboxylase.
XX
XX Hyperthermophilic archaeon; hyperthermophilic protein.
OS Pyrococcus abyssi.
XX
XX FR2792651-A1.
XX
XX 27-OCT-2000.
XX
XX 21-APR-1999; 99PR-0005034.
XX 21-APR-1999; 99PR-0005034.
XX (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
XX
XX Forterre P, Thiery JC, Prieur D, Dietrich J, Lecompte O;
PI Querellou J, Weissenbach J, Saurin D, Heilig R;
XX WPI: 2001-126236/14.
DR
XX
XX New nucleotide sequences isolated from *Pyrococcus abyssi* encode
PT proteins useful in industry -
PT
XX
XX Claim 7: Pages 1298-1300; 1657pp; French.
XX
XX The present invention relates to the genomic sequence of *Pyrococcus*
CC abyssi (see AAF86431 and AAH41223-7) and P. abyssi proteins. P. abyssi is
CC a hyperthermophilic archaeon, which is isolated from deep-sea
CC hydrothermal vents. The present sequence is one such P. abyssi protein.
CC The proteins of the present invention have various potential industrial
CC uses, since the proteins are stable at very high temperatures, some up to
CC 110 degrees centigrade.
CC Note: This patent is in the same patent family as W0200065062, which
CC contains additional sequences as shown in AAB99132-AAB99143,
CC AAH75903-AAH75920 and AAG66436.
XX
SQ Sequence 384 AA:

Query Match 17.3%; Score 514.5; DB 22; Length 384;
Best Local Similarity 30.6%; Pred. No. 3,9e-41;
Matches 121; Conservative 86; Mismatches 164; Indels 25; Gaps 7;

OY 117 PSQGLSSAVLEKLEKYSMDAFMOEGRASGVYSGEKLTELKAYGDPAMNPLHPD 176
DB 5 PEKGLPREVILNLDKTKRVDTLTFSSGKILGSMCMTPH---ELAIEVARYIDRLGDPG 61
OY 177 IFPGRLKTEAEIVRIACSLFNGSGCCVTSCTGTESTIMACKACROLAFEKIGITPREY 236
DB 62 LHPGTRKIEEVEIEMLSDLH-LEKGYGHIVSGTEANILAVRARNTS---DAERPELI 117
OY 237 APOSAAHFAFKKASYFGMKIVRPLTKMNEVDVRRARRAISRTATLVCSPTQPPHGYID 296
DB 118 LPKSHFSTIAGEMLVKLYMAELKQDYADVVKVEAKISDNTIGIYIAGTGLGYVD 177
OY 297 PVPEYAKLAVKKYKIPLVHVDACLGFLIVMEKAGYRLEHDFRVKGVTSIADTHKGY 356
DB 178 DIPALSDLABREGIRLVHDAFGFVIRPAKSLGYDLR-DFDFKLGKGVSTIIDHKKGM 236

QY 357 APKGSGLVLYSDKKYRNYQFVDTDWGGIYASPTIAGSRPGGISAACMAALMHFGENGY 416
D 237 APIPAGGIIFRRKKYLAISVLAAPYLAGKWMQATITGTRPGASVLAVMALIKHLEGEY 296
QY 417 VEATKQIKTARFLAKSLENIKGFVGNQSLIAGSRPDIYRLSNMTAKGWNLN- 475
D 297 REIVRKMEISRWAEIRKLNAMLVREPMLNIVSPQTK-NLRKVERELKRGWGISA 354
QY 476 -----OLQPPPSIHFCITLLHARKRVAIOFLKDIRE 506
D 355 HRGYIRIVFMP-----HVTKEWVEEFLRDIRE 381
RESULT 15
AAV15212
ID AAV15212 standard; Protein; 76 AA.
AC AAV15212;
XX 26-OCT-1999 (first entry)
XX Sphingosine-1-phosphate lyase homologue fragment amino acid sequence.
DE
XX sphingosine-1-phosphate; sphingosine-1-phosphate lyase; SPHINGLY;
KW G-protein coupled receptor; EDG-1; secondary messenger; cancer;
KM cardiovascular disorder; thrombosis; atherosclerosis; wound healing;
XX stroke; apoptosis; homologue; fragment; ds.
OS Homo sapiens.
XX
XX key Location/Qualifiers
FH MISC-difference 42
FT MISC-difference 44 /note= "encoded by NTC"
FT MISC-difference 48 /note= "encoded by NAA"
FT MISC-difference 48 /note= "encoded by NAT"
FT MISC-difference 62 /note= "encoded by NAT"
FT MISC-difference 63 /note= "encoded by ATN"
FT MISC-difference 63 /note= "encoded by GNC"
FT MISC-difference 70 /note= "encoded by NAT"
XX
XX MO938983-A1.
PN
XX
XX 05-AUG-1999.
PD
XX
XX 24-DEC-1998; 98WO-EP08564.
PF
XX
XX 03-NOV-1998; 98GB-0024026.
PR
XX 29-JAN-1998; 98EP-0300625.
XX
XX (SMIK) SMITHKLINE BEECHAM PLC.
PA
XX
XX Duckworth DM, Godden RJ, Testa TT;
PI
XX
XX WPI; 1999-479192/40.
DR N-PSDB; AA206343.
DR
XX
XX A new sphingosine-1 phosphate lyase useful for diagnosing and
PT treating cancers, cardiovascular disorders, thrombosis or
PT atherosclerosis
PS
XX
XX Claim 18; Page 24; 37pp; English.
XX
XX This is the amino acid sequence of the Sphingosine-1-phosphate
CC lyase homologue fragment. The lyase catalyses the cleavage of
CC Sphingosine-1-phosphate to give a long chain aldehyde and
CC phosphoethanolamine.
CC The sequence has use as a method of treating cancers, cardiovascular
CC disorders, thrombosis, atherosclerosis and other conditions. This is due
CC to the action of Sphingosine-1-phosphate intracellularly as a secondary

CC messenger and extracellularly as a ligand for the G-protein coupled
CC receptor EDG-1.
XX
SQ Sequence 76 AA:
QY 467 MTAKGWNLNOLQPPPSIHFCITLLHARKRVAIOFLKDIRESVIOIMKPKATTGMCATY 526
D 1 MTAKGWNLNOLQPPPSIHFCITLLHARKRVAIOFLKDIRESVITKIMKPKATTGMCATY 60
QY 527 AMAQTVDKNNVVEL 541
D 61 GIDQTVDRNNVGR 75

Search completed: October 6, 2003, 13:49:46
Job time : 52 secs

1

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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:39:24 ; Search time 57 seconds
(without alignments)
2571.472 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLMKAFEPYLEILE.....LYSTDPTVQSGQNMNSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues
Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_protist:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2959	99.4	580	4	Q9UG68
2	2950	99.1	568	4	Q95470
3	2567	86.2	568	11	Q8CHN6
4	2557	85.9	568	11	Q8ROX7
5	2553	85.8	568	11	Q54955
6	2551	85.7	568	11	Q8C942
7	1344	45.1	545	5	Q9V772
8	1082	36.3	552	5	Q9Y194
9	1069	35.9	544	10	Q9C509
10	1052	35.3	576	3	Q8X074
11	1025	34.4	557	10	Q93V78
12	1008	33.9	542	5	Q17456
13	1007.5	33.8	589	3	Q05567
14	882	29.6	606	5	Q966E7
15	669	22.5	488	17	Q28946
16	621.5	20.9	414	17	Q27989

17	567.5	19.1	454	17	Q9Y9M1	Q9Y9M1 aeropyrum p
18	549.5	18.5	473	17	Q9Y6B1	Q9Y6B1 aeropyrum p
19	518.5	17.4	383	17	Q58679	Q58679 pyrococcus
20	514.5	17.3	384	17	Q9UZD5	Q9UZD5 pyrococcus
21	511	17.2	371	17	Q8U1P6	Q8U1P6 pyrococcus
22	482	16.2	363	17	Q27188	Q27188 methanobact
23	422	14.2	398	17	Q8PYX5	Q8PYX5 methanosarc
24	393.5	13.2	395	17	Q8TUQ9	Q8TUQ9 methanosarc
25	380	12.8	367	17	Q28275	Q28275 archaeoglob
26	337	11.3	372	17	Q8TV92	Q8TV92 methanopyru
27	315	10.6	468	17	Q8TPG4	Q8TPG4 methanosarc
28	308.5	10.4	355	17	Q9HSA3	Q9HSA3 halobacteri
29	269	9.0	464	16	Q8XIO6	Q8XIO6 clostridium
30	258.5	8.7	125	10	Q8LEF9	Q8LEF9 arabidopsi
31	253.5	8.5	460	16	Q06249	Q06249 mycobacteri
32	244	8.2	500	10	Q9AR41	Q9AR41 cryza sativ
33	239.5	8.0	304	16	Q8YBJ0	Q8YBJ0 bruceella me
34	237.5	8.0	489	16	Q8FNG5	Q8FNG5 escherichia
35	234.5	7.9	464	2	Q8GFI5	Q8GFI5 edwardsiell
36	233.5	7.8	496	10	Q81102	Q81102 nicotiana t
37	230.5	7.7	514	3	Q9UVJ7	Q9UVJ7 aspergillus
38	230	7.7	494	10	Q944L6	Q944L6 arabidopsi
39	229.5	7.7	496	10	Q8LKR4	Q8LKR4 nicotiana t
40	229.5	7.7	520	3	Q8XOB0	Q8XOB0 neurospora
41	228.5	7.7	496	10	Q81101	Q81101 nicotiana t
42	226.5	7.6	496	10	Q9AT17	Q9AT17 nicotiana t
43	225.5	7.6	496	10	P93369	P93369 nicotiana t
44	225	7.6	419	10	Q8RXH0	Q8RXH0 arabidopsi
45	217.5	7.3	467	16	P73043	P73043 synechocyst

ALIGNMENTS

RESULT 1	ID	Q9UG68	PRELIMINARY;	PRT;	580 AA.
AC	Q9UG68	Q9UN89;			
DT	01-MAY-2000	(TREMBLREL. 13, Created)			
DT	01-MAY-2000	(TREMBLREL. 13, Last sequence update)			
DT	01-OCT-2002	(TREMBLREL. 22, Last annotation update)			
DE	Hypothetical protein KIAA1252 (Sphingosine-1-phosphate lyase)				
DE	(EC 4.1.2.27) (Fragment).				
GN	KIAA1252 OR SPL.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain;				
RX	MEDLINE=20039619; PubMed=10574462;				
RA	Nagase T., Ishikawa K., Kikuno R., Hirose M., Nomura N., Ohara O.;				
RT	"Prediction of the coding sequences of unidentified human genes. XV. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro."				
RT	DNA Res. 6:337-345(1999).				
RL	[2]				
RN	SEQUENCE OF 13-580 FROM N.A.				
RP	Zhou J., Saba J.;				
RA	"Cloning and characterization of human sphingosine-1-phosphate lyase gene."				
RT	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.				
RL	Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.				
CC	-1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).				
CC	-1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).				
CC	EMBL; AB033078; BAA6566.1; -				
DR	EMBL; AF14638; AAD4755.1; -				
DR	GeneW; HGNC:10817; SGP1.				
DR	InterPro; IPR002129; Pyridoxal-dec.				
DR	Pfam; PF00282; Pyridoxal-dec. 1.				
KW	Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.				
FT	NON_TER	1	1		

SQ SEQUENCE 580 AA; 64961 MW; 7B18137B02DA65C9 CRC64;
 Query Match 99.4%; Score 2959; DB 4; Length 580;
 Best Local Similarity 99.5%; Pred. No. 1.1e-242;
 Matches 565; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEYV 60
 |||||
 DB 13 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEYV 72
 OY 61 FQPELSMSRFFKKCFELTRKMPILIGRKIDDKLTKTDIDSKNMSFLKVKVEYKALPSOG 120
 |||||
 DB 73 FQPELSMSRFFKKCFELTRKMPILIGRKIDDKLTKTDIDSKNMSFLKVKVEYKALPSOG 132
 OY 121 LSSSAVLEKLEKESMDAFMOEGRASGTYSGEKEKTELLVYKAGDFAMSNPLHPDIFPG 180
 |||||
 DB 133 LSSSAVLEKLEKESMDAFMOEGRASGTYSGEKEKTELLVYKAGDFAMSNPLHPDIFPG 192
 OY 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKARDLAEKGIKTPPEIYAPQS 240
 |||||
 DB 193 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKARDLAEKGIKTPPEIYAPQS 252
 OY 241 AHAFAFKKASYFGMKIVRPVPLTKMMEVDVRAAMRAISRNTAMLYCSTPQPHGVDPVPE 300
 |||||
 DB 253 AHAFAFKKASYFGMKIVRPVPLTKMMEVDVRAAMRAISRNTAMLYCSTPQPHGVDPVPE 312
 OY 301 VAKLAVKXKIPLVHVDACLGFLIVMEKAGYPLEHFDPRVKVGTISADTHKYGAPKG 360
 |||||
 DB 313 VAKLAVKXKIPLVHVDACLGFLIVMEKAGYPLEHFDPRVKVGTISADTHKYGAPKG 372
 OY 361 SSLVLYSDKKRYNYQFVDTMOGGIYASPTIAGSRPGISAAWMAALMHFENGVEAT 420
 |||||
 DB 373 SSLVLYSDKKRYNYQFVDTMOGGIYASPTIAGSRPGISAAWMAALMHFENGVEAT 432
 OY 421 KOIKTARFLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 |||||
 DB 433 KOIKTARFLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 492
 OY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAVE 540
 |||||
 DB 493 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAVE 552
 OY 541 LSSVFLDSLSTDTYVTOGSGMNGSPKPH 568
 |||||
 DB 553 LSSVFLDSLSTDTYVTOGSGMNGSPKPH 580

RESULT 2
 095470
 ID 095470 PRELIMINARY; PRT; 568 AA.
 AC 095470;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
 DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA MEDLINE-20471968; PubMed-11018465;
 RA Van Veldhoven P.P., Gijssbers S., Mannaerts G.P., Vermeesch J.R.,
 Brys V.;
 *Human sphingosine-1-phosphate lyase : cDNA cloning, functional
 RT expression studies and mapping to chromosome 10q22.*;
 RL Biochim. Biophys. Acta 1487:128-134(2000).
 CC -1-COFACITOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1-SYMLARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
 CC TYRDC).
 DR EMBL: AJ011304; CAA09590.2; -;
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.

KW Decarboxylase; Lyase; Pyridoxal phosphate.
 SQ SEQUENCE 568 AA; 63491 MW; 113CFAD4F6C41AA CRC64;
 Query Match 99.1%; Score 2950; DB 4; Length 568;
 Best Local Similarity 99.3%; Pred. No. 6.1e-242;
 Matches 564; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEYV 60
 |||||
 DB 1 MSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPMQILAMSVVMTLLVWGVEYV 60
 OY 61 FQPELSMSRFFKKCFELTRKMPILIGRKIDDKLTKTDIDSKNMSFLKVKVEYKALPSOG 120
 |||||
 DB 61 FQPELSMSRFFKKCFELTRKMPILIGRKIDDKLTKTDIDSKNMSFLKVKVEYKALPSOG 120
 OY 121 LSSSAVLEKLEKESMDAFMOEGRASGTYSGEKEKTELLVYKAGDFAMSNPLHPDIFPG 180
 |||||
 DB 121 LSSSAVLEKLEKESMDAFMOEGRASGTYSGEKEKTELLVYKAGDFAMSNPLHPDIFPG 180
 OY 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKARDLAEKGIKTPPEIYAPQS 240
 |||||
 DB 181 LKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACAKARDLAEKGIKTPPEIYAPQS 240
 OY 241 AHAFAFKKASYFGMKIVRPVPLTKMMEVDVRAAMRAISRNTAMLYCSTPQPHGVDPVPE 300
 |||||
 DB 241 AHAFAFKKASYFGMKIVRPVPLTKMMEVDVRAAMRAISRNTAMLYCSTPQPHGVDPVPE 300
 OY 301 VAKLAVKXKIPLVHVDACLGFLIVMEKAGYPLEHFDPRVKVGTISADTHKYGAPKG 360
 |||||
 DB 301 VAKLAVKXKIPLVHVDACLGFLIVMEKAGYPLEHFDPRVKVGTISADTHKYGAPKG 360
 OY 361 SSLVLYSDKKRYNYQFVDTMOGGIYASPTIAGSRPGISAAWMAALMHFENGVEAT 420
 |||||
 DB 361 SSLVLYSDKKRYNYQFVDTMOGGIYASPTIAGSRPGISAAWMAALMHFENGVEAT 420
 OY 421 KOIKTARFLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 |||||
 DB 421 KOIKTARFLKSELENIKIFVFGNPQLSLIALGSDPDYIRLSNMTAKGNLNOLOPP 480
 OY 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAVE 540
 |||||
 DB 481 PSIHFCITLLHARKRAVIOFLKDIRESVQIMKNPRAKTGTGAIYAMAQTTVDNRMAVE 540
 OY 541 LSSVFLDSLSTDTYVTOGSGMNGSPKPH 568
 |||||
 DB 541 LSSVFLDSLSTDTYVTOGSGMNGSPKPH 568

RESULT 3
 08CHN6
 ID 08CHN6 PRELIMINARY; PRT; 568 AA.
 AC 08CHN6;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN (1)
 RP SEQUENCE FROM N.A.
 RA Van Veldhoven P.P.;
 Comparison of sphingosine-1-phosphate lyases.;
 RT Submitted (OCT-2002) to the EMBL/Genbank/DBJ databases.
 RL EMBL: AJ512838; CAD55407.1; -;
 DR Lyase.
 KW
 SQ SEQUENCE 568 AA; 63758 MW; A0B59A072CC79F48 CRC64;
 Query Match 86.2%; Score 2567; DB 11; Length 568;
 Best Local Similarity 85.2%; Pred. No. 2.3e-209;
 Matches 463; Conservative 36; Mismatches 48; Indels 0; Gaps 0;

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QY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVNGCHCTKEPMMOLIAVYVTLIIYGEYEV 60
DB 1 MPSTDLMLKDFEPELEILEYVSTKAKNVNGCHCTKEPMMOLIAVYVTLIIYGEYEV 60
QY 61 FOPESLMSRFKKKFKLTKRMKPIIGRKIQDKLNTKDDISKNMSEFLKYDKEYKALP50G 120
DB 61 FOPESLMSRFKKKFKLTKRMKPIIGRKIQDKLNTKDDISKNMSEFLKYDKEYKALP50G 120
QY 121 LSSAVLEKLEKESMDAFWOGGRASGTVSGEEKLTLLYKAYDFAMSNPLHPDIPG 180
DB 121 LSTAEVLRLKEYSMDVFWOGGRASGTVSGEEKLTLLYKAYDFAMSNPLHPDIPG 180
QY 181 LRKLEAEIVRIACSLFNGGPDSCGCVTSGTESILMACACRDALFEKGIKPELIVAPES 240
DB 181 LRKLEAEIVRIACSLFNGGPDSCGCVTSGTESILMACACRDALFEKGIKPELIVAPES 240
QY 241 AHAAPNKAASYFGMKIVVPLTKMWEVDVRAKRAISRNTAMLVCSFQPPHGVIDPYE 300
DB 241 AHAAPNKAASYFGMKIVVPLTKMWEVDVRAKRAISRNTAMLVCSFQPPHGVIDPYE 300
QY 301 VAKLAVKXKIPPLHDACGGLIYFMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
DB 301 VAKLAVKXKIPPLHDACGGLIYFMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
QY 361 SSVLVSPDKKRYNFOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHFGENGVEAT 420
DB 361 SSVLVSPDKKRYNFOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHFGENGVEAT 420
QY 421 KOIKTARFLKSELENIKGIFVGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOIKTARFLKSELENIKGIFVGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
QY 481 PSIHCTTLTARKKVAIOFLKDIRESYTOIMKNPKATGTGMAIYAAQTTVDNRVAE 540
DB 481 PSIHCTTLTARKKVAIOFLKDIRESYTOIMKNPKATGTGMAIYAAQTTVDNRVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567

RESULT 4
Q8ROX7 PRELIMINARY: PRT: 568 AA.
AC Q8ROX7:
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Sphingosine phosphatase 1.
GN SCPL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Liver:
RA Strausberg R.;
RN Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
RL [2]
RN SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Bone, and Thymus;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RL Nature 420:563-573(2002).
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (PDC, GAD, HDC AND
CC TYRDC).
DR EMBL; BC026135; AAH26135.1; -.
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DR EMBL; AK036747; BAC29562.1; -.
DR EMBL; AK037789; BAC39872.1; -.
DR EMBL; AK049342; BAC33695.1; -.
DR MGD; MGI:1261415; Sgpl1.
DR InterPro; IPR002129; Pyridoxal_dec.
DR Pfam; PF00282; Pyridoxal_dec; 1.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 568 AA; 63677 MW; FASD52E4E89D09E CRC64;

Query Match 85.9%; Score 2557; DB 11; Length 568;
Best Local Similarity 84.3%; Pred. No. 1.6e-208;
Matches 478; Conservative 43; Mismatches 46; Indels 0; Gaps 0;

QY 1 MPSTDLMLKAFEPYLEILEYVSTKAKNVNGCHCTKEPMMOLIAVYVTLIIYGEYEV 60
DB 1 MPSTDLMLKDFEPELEILEYVSTKAKNVNGCHCTKEPMMOLIAVYVTLIIYGEYEV 60
QY 61 FOPESLMSRFKKKFKLTKRMKPIIGRKIQDKLNTKDDISKNMSEFLKYDKEYKALP50G 120
DB 61 FOPESLMSRFKKKFKLTKRMKPIIGRKIQDKLNTKDDISKNMSEFLKYDKEYKALP50G 120
QY 121 LSSAVLEKLEKESMDAFWOGGRASGTVSGEEKLTLLYKAYDFAMSNPLHPDIPG 180
DB 121 LSSAVLEKLEKESMDAFWOGGRASGTVSGEEKLTLLYKAYDFAMSNPLHPDIPG 180
QY 181 LRKLEAEIVRIACSLFNGGPDSCGCVTSGTESILMACACRDALFEKGIKPELIVAPES 240
DB 181 LRKLEAEIVRIACSLFNGGPDSCGCVTSGTESILMACACRDALFEKGIKPELIVAPES 240
QY 241 AHAAPNKAASYFGMKIVVPLTKMWEVDVRAKRAISRNTAMLVCSFQPPHGVIDPYE 300
DB 241 AHAAPNKAASYFGMKIVVPLTKMWEVDVRAKRAISRNTAMLVCSFQPPHGVIDPYE 300
QY 301 VAKLAVKXKIPPLHDACGGLIYFMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
DB 301 VAKLAVKXKIPPLHDACGGLIYFMEKAGYPLEHPFRKGVTSISADTHKGYAPKG 360
QY 361 SSVLVSPDKKRYNFOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHFGENGVEAT 420
DB 361 SSVLVSPDKKRYNFOFVDTMOGGIVASPTIAGSRPGISAAACAAALMHFGENGVEAT 420
QY 421 KOIKTARFLKSELENIKGIFVGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
DB 421 KOIKTARFLKSELENIKGIFVGNPOLSLIALGSRDPIYRLSNLMTAKGNLQLOFP 480
QY 481 PSIHCTTLTARKKVAIOFLKDIRESYTOIMKNPKATGTGMAIYAAQTTVDNRVAE 540
DB 481 PSIHCTTLTARKKVAIOFLKDIRESYTOIMKNPKATGTGMAIYAAQTTVDNRVAE 540
QY 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567
DB 541 LSSVFLDSLSTDTVTOGSONMGSPKP 567

RESULT 5
Q54955 PRELIMINARY: PRT: 568 AA.
AC Q54955:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Sphingosine-1-phosphate lyase (EC 4.1.2.27).
GN SCPL1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=96125521; PubMed=9464245;
RA Zhou J., Saba J.D.;
RT "Identification of the first mammalian sphingosine phosphatase lyase
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazel R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Agbayan A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bokova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Butts J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahke C., Davenport L.B., Davies P.,
RA De Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunham B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gloder A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Jatalil M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mishina N.V., Moharry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclob J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissensbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RA "the genome sequence of *Drosophila melanogaster*.";
RL Science 287:2185-2195(2000).
RN [2]
RA SEQUENCE FROM N.A.
RP Van Veldhoven P.P.;
RT "Functional expression of sphingosine-phosphate lyase from *Arabidopsis*
RT and *Drosophila*.";
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RA SEQUENCE FROM N.A.
RP Stapleton M., Brokstein P., Hong L., Abmayan A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Farfan D., Fise E., George R.,
RA Gonzalez M., Guatin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nuno J., Paclob J., Paragas V., Park S., Phouanavong S., Wan K.,
RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC TYRDC).
CC EMBL: AE003804; AAF57903.1; -;
DR EMBL: AJ297394; CAC10531.1; -;
DR EMBL: AY052075; AAK93499.1; -;
DR FLYBASE: FBgn0010591; SPLY.
DR InterPro: IPR002129; Pyridoxal_dec.
DR Pfam: PF00282; pyridoxal_dec; 1.
KW Decarboxylase; Lyase; Pyridoxal phosphate.
SQ SEQUENCE 545 AA; 60305 MW; 26000F4AE43F85FD CRC64;

Query Match 45.1%; Score 1344; DB 5; Length 545;
Best Local Similarity 49.0%; Pred. No 2.2e-105; Indels 4; Gaps 4;
Matches 254; Conservative 100; Mismatches 160;

QY 38 EPMQILAMSVYVTLIIWGYEFVQPESLMSRFKKCKELTKRMPTIGRKIQDKLNKTKD 97
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 25 EPMQVATITATVTVGVWLVVICODENLIRGRQKPFKAKKIPAVARQVETELAKAKN 84
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 98 DISKMSFLKVDKSVKALPSQGLSSAVLEKLEKEYSSMDAF-WQEGASGVTSGEKEL 156
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 85 DFETRIKSNMHLTYSETLPKGLSKKEILRLVDEHLTKGHYNMRDGVSGAVGYKPKDL 144
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY 157 TELLVKAAGDEAWNSNPLHPDIFPGLRKIEAIVRIACSLFNGGPDSCGCVTSGETSTIM 216
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 145 VELVTEVYKSAKSYNPLHADLPQGVCKMEAVVRMACLHPGNSASCTMTGTGTESTIVM 204
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 217 ACKACRDLAEF-KGIKTPEIYAPOSAHAAEFKAASFQMKIVRPDL-TKMEEDVVRAMRR 274
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 205 AMKAVRFQFARFKYKITTNRNIVVPTVHAAPFGKGOYFHNRSVDVDETEYVDKKRKR 264
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 275 AISRNTALVCSQFPQFPGVDPPEVAKLVKKYKIPHYDACLGFLIVMEKAGPYLE 334
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 265 AINRNTLLVGSAPNPFYGTITDDIEALNALGVKTDIPVHDAVCLASFVALVRNAGYTL- 323
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 335 HPDFERYKGVYSISADTHKYGAPKSSLVLYSDKRYKNRYOFVDTMOGGIYASPTIAG 394
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 324 RPFPEYKGVYSISADTHKYGAPKSSLVLYSDKRYKNRYOFVDTMOGGIYASPTIAG 383
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 395 SRPGISACAAALMHGEGNVYENTKOIITAPRLKSELENIGKIFVGNPQSLIALG 454
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 384 SRAGGIYAACWATMMSFGYDGLATKRIYDTARIENGVRDIDGIFFGKPRATSVIALG 443
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 455 SRDDIVRLSLMTRAKGNLMOLOPPSIHCITLLHARKRVAIOFLKDIRESYVQIMKN 514
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 444 SNVEDIEFLSDSLCKLGNLALPSPGICHLCTVDMHQPGVADKFIADVRSCTAEIMKD 503
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
QY 515 PRAKTTGKAIYAMAQTTVDNRNVAELSSVFLDSLYST 552
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
DB 504 PGQPVYGMKALYGMAGQSIPIRDSVIGEYRLRLHSMYTY 541
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

RESULT 8
ID 09Y194 PRELIMINARY; PRT; 552 AA.
AC 09Y194;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE SPHINGOSINE-1-phosphate aldolase (EC 4.1.2.27).
GN SPL OR Y66H1B.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RX [1]
RA SEQUENCE FROM N.A.
RP Zhou J., Saba J.;
RT "Cloning and characterization of *C. elegans* sphingosine-1-phosphate
RT lyase gene.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RA SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC MEDLINE-94150718; PubMed=7906398;
RX WILSON R., Alnscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lightning J., Lloyd C., McMurray A., Mottimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownteen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierley-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstein L., Wilkinson-Sproul J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of *C.*
RT elegans.";
RL Nature 368:32-38(1994).
RN [3]
RA SEQUENCE FROM N.A.
RP STRAIN-BRISTOL N2;
RC Clarke K., Wohlmann P.;
RT "The sequence of *C. elegans* cosmid Y66H1B.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RN [4]


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Db 186 LLSKETASGGQICGNTSGTESIVLAVSSRDYMKKGTREPMIIPESGHSAYDKA 245
QY 249 ASYEGMKIVRPLTKMEVVDVRAAMRAISRNTAMLVOSTPOFPHGVIDPVEVAKLAVKY 308
Db 246 AQFVKITLMKRVVDKDRADYKATRRHINNTIMIVGSAPEFPGIITDPIELQOLALSY 305
QY 309 KIPLHVDACLGLFVIVEMERAGYPLEHPDFRVRKVSISADTHKYAPKSSLYVYSYD 368
Db 306 GICHHVDLCGLGFVLPFAKRIKGYQIP-PFDSVGVGVSISVDVHKYGLAPRGSTVLYRN 364
QY 369 KKRNYOFPVDTMOGGITVSPITAGSRPGCISAAACNAALMHGENGVEATKOIYKAR 428
Db 365 HEIKRHOFAVTEWMSGGLYVSPITAGSRPGSLVAGAAAMMSLGEEGYLOQTSKIMEASK 424
QY 429 FLKSELNINIGIFVFGNPDQLSLAGSRDPIYRLSLMTRAKGNLNLQLOPPSIHFCIT 488
Db 425 RLEGVREIHELFEYIGRPMITVAFGSKALDIEFVNDIMSKGHLNALOPNSIHICIT 484
QY 489 LILHARKKVAIOFLKDIESVYTOIKMNPRAKTTGCAIYAMAQTVDRNMVAELSVFLDS 548
Db 485 LQHY--PVVDDELFLDLREAVETVKANPGITGGLAPIYGAAGKMPDRGMVELLVTFMDS 542
QY 549 LY 550
Db 543 QY 544

RESULT 10
08X074 ID 08X074 PRELIMINARY; PRT; 576 AA.
AC 08X074;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Probable sphingosine-1-phosphate lyase.
GN B14D6.540.
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN RN
RP SEQUENCE FROM N.A.
RA Schulte U., Algen V., Hohelsel J., Brandt P., Fartmann B., Holland R.,
RA Nyakatura G., Mewes H.W., Mannhaupt G.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Geomys Neurospora genome project;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR EMBL: AL356173; CAB91763.2; -.
DR InterPro: IPR001092; HLH_Basic.
DR InterPro: IPR002129; Pyridoxal_dec.
DR Pfam: PF00282; Pyridoxal_dec.1.
DR PROSITE: PS00038; HLH.1; 1.
KW Decarboxylase; lyase; Pyridoxal phosphate.
SQ SEQUENCE 576 AA; 63519 MW; EDFZCDB33BB41A7 CRC64;

Query Match 35.3%; Score 1052; DB 3; Length 576;
Best Local Similarity 41.9%; Pred. No. 1.6e-80;
Matches 224; Conservative 115; Mismatches 154; Indels 42; Gaps 16;

QY 49 WTLLIIVG-----YEVFQPEISMSRKKCFKLTAKPIIGKRIQDKLTKTODISK- 101
Db 49 WTRRALKMLKRGFLGLE---LFTDARILLYGYFRLPGRVRAQID---DALTKM 102
QY 102 NMSFLKVDKEXVKALPSQGLSSAVLEKLEKYSMD-AFMQEGRASVYSGEKEITELL 160
Db 103 QAKIIPACQIYIYSLPREGWTEEVARKLELALATMDTRKWDGYVSGAVSGEDELKIQ 162
QY 161 VKAYGDFWASNPDLHPDIFPGLRKIEAIVRIACSLFNGGPDSCGVTSGTESIIMACKA 220

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Db 163 TEAYGKFTVANPIHPDVEPVGKMEAEVVAALVLSLFNAPGAAAGVSTSGTESIIMAILS 222
QY 221 CRDLAF-EKGKTPETIYAPOSANAENKASYSFEMK--YRVPLTKMEVDVRAAMRAIS 277
Db 223 AROKAYHERGVEEEMIIPEFAHTAFKRAEYFNKILHLVACP-APTYQVDTKRVAVLI 281
QY 278 RNTAMLVCSNPQPHGVIDPVEVAKLAVKPKIPLHVDACLGLFVIVEMERAGYPLEHPF 337
Db 282 RNTIMLVGSAPNPFHGIIIDDISALSKLARKKPIPLHVDCCLGSTLVPLDAGD-SQPF 340
QY 338 DFRVKGVTISADTHKGYAPAKGSSLVLYSDKRYRNYOFVDTMOGGITVSPITAGSRP 397
Db 341 DFRKGVTSISCDPHKKGAFAPKNSVLYRYRAELRSYQYFVDPMSGSGVYASPGIAGSRP 400
QY 398 GGISAACMAALMHGENGVEATQIIT---KTRAFKSELNINIGIFVGNPDLSIAL 453
Db 401 GALIACWASIMSGEGGYLKSCTQIYGARKKLAELHRSHTLOQEEIILNPLVSVLAF 460
QY 454 GSR-DPDIYRLSLMTRAKGNLNLQLOPPSIHFCITLILHAR--KRAVIOFLKDI----- 504
Db 461 QARGDLNITYDIADGMSRGMHLNLQNPRAIHVAVTAPVAKNMERLA-QDEGVVEERE 519
QY 505 RESVTQIM-----KNPRAKTTG-MGAIYAMAQTVDRNMVAELSVFLDSLY 550
Db 520 KERVRQVEALKMGISGKTGKOKAGDTAALYGVAGSLPKNKSVVVDLARGFLDLLY 574

RESULT 11
093VF8 ID 093VF8 PRELIMINARY; PRT; 557 AA.
AC 093VF8;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DE 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Putative sphingosine-1-phosphate lyase.
GN P0672D08.7 OR P0402A09.4.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN RN
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0672D08."
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=cv. Nipponbare;
RC STRAIN=cv. Nipponbare;
RA Sasaki T., Matsumoto T., Yamamoto K.;
RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
RT clone:P0402A09."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
DR EMBL: AP003727; BAB64236.1; -.
DR EMBL: AP003610; BAB62623.1; -.
DR Gene: 093VF8; -.
DR InterPro: IPR002129; Pyridoxal_dec.
DR Pfam: PF00282; Pyridoxal_dec.1.
KW Decarboxylase; lyase; Pyridoxal phosphate.
SQ SEQUENCE 557 AA; 60536 MW; C21CEC17B7D6198 CRC64;

Query Match 34.4%; Score 1025; DB 10; Length 557;
Best Local Similarity 39.5%; Pred. No. 3e-78;
Matches 223; Conservative 103; Mismatches 190; Indels 48; Gaps 12;

QY 22 YSRKAKNVNGCHCTKYPEWOLIAWSVYVWTL--IYVGEFVQPEISMSRKKCFKRLTR 79

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DB      3 FALRLDAAHHLSRYEPLVLLAALLAARLTHAAAAAADAADRLTVLLALAMTAIK 62
QY      80 KMPIIGRKIDQLNKTKDID-----SKNMSFLVKDEYVAKLPSSGLSSAVLEKLEKYES 135
DB      63 LEPGSAYINAKRKRVVDQLQSGGSTSTKLTRE-----LPTVGLSNQ-VINDELTAKA 115
QY      136 MAFNOEGASGTVY----SGEEKLELLVKAAGDFAWSPNLPDIFPGIRKIDAEIVRIA 192
DB      116 RQVNMQ-GKSGSTVIYAGSESEGHFALINKAYSMESHPLQDVFYSVAOLEAEVYVAMT 174
QY      193 CSLF-----NGPDSGCVTSGTESILMACACRD-LAFEGIKRPEIVAPQSAHAAN 246
DB      175 AALLGTRKESSGGQICGNMTSGTESILAVKTSRDYMTKKGIRKPEMILIAESAYD 234
QY      247 KAASYFGMKIVRPLTKMEVDVRAARRAISRTAMLVGSTPOFPHGVIDPYEVAKLAV 306
DB      235 KAAQGFNIKVRVPVAKKEFLADVKGFKRCINGNTIMVGSAPGPFGLDIPBELGELAS 294
QY      307 KKKIPLHVDACLGFLIYMEKAGYPLEHPDPRKVCVTSISADTHKYGAPKGSGLVY 366
DB      295 RDICLHVDLCGFLVLPFARKIGYPIP-PEDFCVKGVTSISTDVHKYGLAPKGSIVLY 353
QY      367 SDKKYR-----NQGFVD-----TDMOGGIYASPTINGSRPGISAC 404
DB      354 KHEIRKISWLSLHNTYSLTDMIMQNTKMFQYTEMVGLYVSTIAGSRPGILAGA 413
QY      405 MAALMHFENGVEATKQIITKARFLKSELENIKGIFVGNPOLSLIALGSRDFDIYRLS 464
DB      414 WAAAMSLGNGYMEWNTGHMEVSKIKQRIEDIPGLFVIGKRDYMTVAAGSSVDIEFN 473
QY      465 NIMTKAGNINLOFPPIHFCITLLHARKVAQLFDKIDRESVTOIMKPKAKTTGMA 524
DB      474 DIMSSGWHNLQSPNSLHICVTLOHT--VIYEELKDLKDSVDTVKANPGPISGRAP 531
QY      525 IYAAQTVDRMVAELSSVFLDS 548
DB      532 IYGAAGKMPDRGMRELLVEFMDA 555

RESULT 12
017456 PRELIMINARY; PRT; 542 AA.
AC      017456:
DB      01-NOV-1996 (TREMBLrel. 01, Created)
DB      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DB      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Hypothetical 61.1 kDa protein.
GN      B0222.4
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OX      Rhabditidae; Peloderinae; Caenorhabditis.
RN      NCBL_TaxID=6239;
RP      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RX      MEDLINE=990613; PubMed=9851916;
RA      None;
RT      Genome sequence of the nematode C. elegans: a platform for
RT      investigating biology. The C. elegans Sequencing Consortium.
RT      Science 287:2012-2018(1998).
RN      [2]
RN      SEQUENCE FROM N.A.
RN      STRAIN-Bristol N2;
RN      Du 2., Gattung S.;
RT      "The sequence of C. elegans cosmid B0222."
RT      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN      [3]
RN      SEQUENCE FROM N.A.
RN      STRAIN-Bristol N2;
RN      Waterston R.;
RT      "Direct Submission."
RT      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC      -I- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).

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CC      -I- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND
CC      TYRDC).
DR      EMBL: U50312; AAA92321.1; -.
DR      Wormpep: B0222.4; GE06699.
DR      Interpro: IPR002129; Pyridoxal_dec.
DR      Interpro: IPR006025; Zn_MTPeptide.
DR      Pfam: PF00282; pyridoxal_dec; 1.
DR      PROSITE: PS00142; ZINC_PROTEASE; 1.
KW      Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.
SQ      SEQUENCE 542 AA; 61133 MW; 3EB9A3082A8A426 CRC64;

Query Match      33.9%; Score 1008; DB 5; Length 542;
Best Local Similarity 38.1%; Pred. No. 8, 1e-77;
Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

QY      19 LEVYSKRAKNYVNGCHTKREPQNLAMSVVWLLIYWGVEFQEPESLSRKKCKFKT 78
DB      5 LEQYHS-AKDLIFELRKNPVLVSVTVIATVYVTLNRHMLHDEGIRKRLSTFEFTTV 63
QY      79 KMPIIGRKIDQLNKTKDIDSKNMSFLVKDEYVAKLPSSGLSSAVLEKLEKYESMDA 138
DB      64 KRVPIFKKIDQLNEVDKLEKSLRIYDRSTREYFTTISHSVGREYRLAATYDDEG 123
QY      139 -FWQGRASGTYSGBEKL--TELLKAYGDFAWSPNLPDIFPGIRKIDAEIVRIASL 195
DB      124 PAFLGGRVSGAVFNRDDKDEREMYEYGFKAFTNPMPKLPFGVRIAEAVHRCMM 183
QY      196 FNGSPDSCGCVSSGSESTIMACKCRDLAFKGIKTPETIVAPQSAHAAFKAAFGMK 255
DB      184 MNGDSETCGTSTGGISITLLACLAHRNRLRGEYTEMIVPSSHAAFFFAACFRK 243
QY      256 IYRVPLTKM-MEVDVRAARRAISRTAMLVGSTPOFPHGVIDPYEVAKLAVKRIPLHV 314
DB      244 VKRIPDPTFVFDLVKKMAALINKRCMLVGSAPNPEFTVDIEIGLGLEYDIPHV 303
QY      315 DACLGFLVEMEKAGYPLEHPDPRKVCVTSISADTHKYGAPKGSGLVYSDKKYRY 374
DB      304 DACLGFLVPLEED---EIRYDERVPSVSSISADSHKYGAPKGSGLVLRNKLHLN 359
QY      375 OFEVDPMOGGIYASPTINGSRPGISACMAALMHFENGVEATKQIITKARFLKSEL 434
DB      360 QTFCDADMOGGIYASATMGSRAGHINIALCMAAMLYHNOEGYKAAARKLVDTTKIRNL 419
QY      435 ENIKGIFVFNQPSLIALGSRD-FDIYRLSNIMTKAGNINLOFPPIHFCITLLHAR 493
DB      420 SNIKGKILQSPSDVCISWTNDGVELYEFHFMKEKHQNLGLOFPAGVHIMVNMNTH 479
QY      494 KRVAIQFLKIDRESVTOIM--KNPKAKTTGMAIYAAQTVDRMVAELSSVFLDSLS 551
DB      480 PGLAEAFVADCRAAVEFYKSHKPSSEDKTSEAAIYGLAOSIPDRSLVHEFAHSYIDAVYA 539

RESULT 13
005567 PRELIMINARY; PRT; 589 AA.
AC      005567:
DB      01-NOV-1996 (TREMBLrel. 01, Created)
DB      01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DB      01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE      Similar to glutamate decarboxylase.
GN      DPL1 OR D9819.5 OR YDR294C.
OS      Saccharomyces cerevisiae (Baker's yeast).
OC      Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX      Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
RN      NCBL_TaxID=4932;
RP      SEQUENCE FROM N.A.
RC      STRAIN-S288C;
RA      Fulton L.;
RT      Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
RN      [2]
RN      SEQUENCE FROM N.A.
RN      STRAIN-S288C;

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RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favello A., Fulton L., Gattung S., Greco T., Kitzman J., Kucaba T.,
 RA Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D.,
 RA Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menzies S.,
 RA Miller N., Nhan M., Pauley A., Peluso D., Riken L., Riles L.,
 RA Talch A., Trevisks E., Vignati D., Wilcox L., Wohlman P., Vaudin M.,
 RA Wilson R., Waterston R.,
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RL Waterston R.;
 RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Jia Y., Cherry J.M.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
 DR EMBL: U51031; AAB64470.1; -
 DR SCD; S0002702; DPL.
 DR Interpro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.
 KM Decarboxylase; Lyase; Pyridoxal phosphate.
 SO SEQUENCE 589 AA; 65565 MW; 75FAF8182AF72266 CRC64;

Query Match 33.88; Score 1007.5; DB 3; Length 589;
 Best Local Similarity 39.14; Pred. No. 1e-76;
 Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

QY 51 LLIWGEYF-----VFQPSL-----MSRKKCKFKLRKMPITGRKIOQKLNKTGD 97
 DB 60 LFIYFCKLISNFYLIKVGPRVLAIVTEHSSRRLFRMLDSPELRGTEKEVTKVKQ 119
 QY 98 DISKNSFLKVDKEYK--ALPSQGLSSAVLEKLEKESM--DAFQEGRASGTYVSGE 153
 DB 120 SIDDEL--IRSDSQLNFPOLPSNGIPQDDVIEELNKLNLINHTQKEKVGAYHGG 177
 QY 154 EKTLLVKAIGPANSPLHPDIFPEGLKTEAEIVRIACSLFNGSPDS--CGCVTSGETE 212
 DB 178 DDILHLOTIYERKCVANQLHPDVPFVPRKMESEVSMVLRFNAPSDTGCSTTSGETE 237
 QY 213 SILMKACRDLAF--EKGITPELVAPOSAAHAFNKAASYFGKIYAVPL--TKMEVDVR 270
 DB 238 SLILACLSAKMYALHNRGITPELVAPOSAAHAFNKAASYFGKIYAVPL--TKMEVDVR 297
 QY 271 AMRRASIRNTAMLVCSIPQFPHGVIDPVEPAKLAIVKYLPHVADCLGFLIVEMKAG 330
 DB 298 KVKKFKINKNTILLVGSAPNRPFGIADIEGLKIAQKYKRLPHVDSCLSEIYSPMKAG 357
 QY 331 YPLEHPDFRYKCVTISADTHKYGYAPKSSLVLYSDKKYRNYQFQVDTDMOGGIYASP 390
 DB 358 YKMLPLDFRPVPTGISCDTHKYGFAFKGSSVIMYNSDLRMHQYVNPAMTGGIYGP 417
 QY 391 TINGSPRGISAAQMAALMHFGNGVYEATKOIITKA--RELKSELEIKKIFVFGNPOLS 449
 DB 418 TLGSGRGATLVGCMVMMVNGENGYESCOEIVGAAMKFKYIOENIPLNTMGNRYIS 477
 QY 450 LIALGSRDPIYRLSNLMTAKGNLNLQDPPSIHFCITLLHARKRVAIOFLKDIRESVT 509
 DB 478 VIFSSKTLNIIHLSDBLSKKGMFNALOKRVALHMFRTLSAH---VDEIDCIDLITIV 534
 QY 510 QIMK---NPKAKTTGKATYAMAQTYVDRMVAELSSVFLDSLY---STDVYTO 557
 DB 535 QEIKSESNSKSPDGSATLYGVAGSVYTAGVADKLIVGFLDALYKILGPGEDATK 589

RESULT 14
 Q966E7 PRELIMINARY; PRT; 606 AA.
 AC Q966E7;
 AC Q966E7;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein Y104H12D.3.
 GN Y104H12D.3.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA Waterston R.;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Bauer C., Courtney L., Maupin R.;
 RT "The sequence of C. elegans cosmid Y104H12D.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Bristol N2;
 RA Waterston R.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- COFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
 DR EMBL: AC006701; AAK68403.2; -
 DR WormRep: Y104H12D.3; CE31632.
 DR Interpro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec; 1.
 KM Hypothetical protein; Decarboxylase; Lyase; Pyridoxal phosphate.
 SO SEQUENCE 606 AA; 68135 MW; 4A79F8D4340975CC CRC64;

Query Match 29.68; Score 882; DB 5; Length 606;
 Best Local Similarity 34.68; Pred. No. 5e-66;
 Matches 185; Conservative 116; Mismatches 204; Indels 30; Gaps 5;

QY 31 NGHCTYEPQWLAMSVWTLIIWGEYFQFQPSLSMRKKCKFKLRKMPITGRKIO 90
 DB 29 NACSGLEPQIYSAISCLFLAYIKRMRSDPRLVQIKSTFSLRSLPVRKRLTA 88
 QY 91 KLNKTYADISKNNSFLKVDKEYKALPDSGLSSAVLEKLEKESM--DAFQEGRASGTYV 150
 DB 89 DLAKQAELIDEVHOSDHMRFEYKFLPERCMDEIILADGRRYAM----- 134
 QY 151 SGE-----EKTLLVKAIGDPAWSNPLHPDIFPEGLKTEAEIVRIACSLFNG 198
 DB 135 -GERRRYQHYDPOTREDMKLSAKLFDLFANHPDRSDAPGVKMKAEITLKTCAMFEG 193
 QY 199 GPSCGCVTSGGTESILMKACRDLAEFGKITPELVAPOSAAHAFNKAASYFGKIYR 258
 DB 194 GKSCGCVAGGIGDALMLACLAIRNSRAGBRAEIVASTNHPALDKAAAFEDMTIKR 253
 QY 259 VPLTKME--VDVAMRRARISRNAMLVCSIPQFPHGVIDPVEPAKLAIVKYLPHVAD 317
 DB 254 IOVSEFDDBRANVAMKRAIRPTCMIIASAPNHITGVDPDIEKLAKLAQRYHPLHVDCT 313
 QY 318 LGGFLIVEMKAKAYPLEHPDFRYKCVTISADTHKYGYAPKSSLVLYSDKKYRNYQF 377
 DB 314 LGGFLVLEPMYADYVAP--AFDFRLPGVTISADLHRRGQCGRLSVLMTREPAFLRHQF 372
 QY 378 VDTDMOGGIYASPTIAGSRPGISAAQMAALMHFGNGVYEATKOIITKAIFLKSLENI 437
 DB 373 TNSMPGCGYATPTMSGGRGCGAVATPAMAMMLKKRGDGTINAAORRIEATROLAYRLQGL 432
 QY 438 KGIFVGNPOLSLIALGSRDPIYRLSNLMTAKGNLNLQDPPSIHFCITLLHARKRVA 497
 DB 433 DGVSLRGSADLCVAAFTSEVNVNLYVDVWVGKMHVDPDLSPAARVPISLSMCEGVLY 492

QY 498 IOFLDIRESYTOIKKNPKAKTTGGA-IYANAQTVDRNNVAVELSSVFLDLSYS 551
DB 493 DHFLELDMAICNLKMSKMEPAEIKGTTASFYOMLQVNDKTLVDLSLRLAAHYS 547

RESULT 15

028946 PRELIMINARY; PRT; 488 AA.
AC 028946;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE Group II decarboxylase.
GN AF1323.
OS Archaeoglobus fulgidus.
OC Archaea: Euryarchaeota: Archaeoglobi: Archaeoglobales;
OC Archaeoglobaceae; Archaeoglobus.
OX NCBI_Taxid=2234;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleck H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Fleischmann D.L., Kierlavage A.R., Graham D.E., Kyrpides N.C.,
RA Kirtness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,
RA Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T.,
RA Cotton M.D., Spriggs T., Artlich P., Kalne B.P., Sykes S.M.,
RA Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulphate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -1- CORFACTOR: PYRIDOXAL PHOSPHATE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO GROUP II DECARBOXYLASES (DDC, GAD, HDC AND TYRDC).
CC EMBL: AE001012; AAB89922.1; -.
DR TIGR: AF1323; -.
DR InterPro: IPR000463; Fatty_acid_BP.
DR InterPro: IPR002129; Pyridoxal_dec.
DR Pfam: PF00282; Pyridoxal_dec; 1.
DR PROSITE: PS00214; PABP; 1.
KW Decarboxylase; Hypothetical protein; Lyase; Pyridoxal phosphate;
KW Complete proteome.
SQ SEQUENCE 488 AA; 54562 MW; 84AA3F0AE053CFB6 CRC64;

Query Match 22.5%; Score 669; DB 17; Length 488;

Best Local Similarity 36.5%; Pred. No. 4.6e-48;

Matches 155; Conservative 83; Mismatches 171; Indels 16; Gaps 8;

QY 92 LNKTDIDISKMSFLKAVKEVKALPSQGLSSAVLEKLEKSSMDAFWQEGRASGV-Y 150
DB 10 LNKGGHNSFEVKYIRHTTKIMSPN-GSDAEGVLRLEDAKKNDFPHSRMWHIYY 68
QY 151 SGEKRLTELVAAGDFAMSNPLHPDIPPGLRKIAEIVRIAGSLFNGPDCGCVTSGG 210
DB 69 AGLKVVELARKAYIMYDMKTLDFTCPSLIRMEREVYMASSLLNGDEEVGNFTYGG 128
QY 211 TESILMAKACRDIAFEK--GIKPEIVAPQSAHAFAFNKAASYFGMKIVRPLTKMMEV 267
DB 129 TESILALKAARE-KFRKEGGNVPEIVLPATAPAFWKSAYELGMCLRAKLDELRA 187
QY 268 DYRAMRAISRNTAMLVCTSPQPHGVTDVPEVAKLAVKYLPLHVDACLGGLIYME 327
DB 188 DVEFYKELVGDXTAMIVGSAFNYPGCVDDIKALSDIADVCKLWLHVADACLGGLPFR 247
QY 328 KAGVLEHPDFPRVAVTSISADTFHKYGAAPKSSLVYSKKYRNVQFFVDTMGGIY 387
DB 248 ELGEKIP-DFDSVYEGVHSHSADFHRYGLSPGASVILYRNKALREGQIFVWASMPGYPL 306

QY 368 ASPTIAGSRPGISACAAALMHFGENGCVYEAATKOIITAPRLKSELENIGIFVGNPQ 447
DB 307 VNTAVLSTRSAGTILAAAWAVMSYIGFDGYLKLAKKTLVAKKRLIDGLTEL-GLLELGSPE 365
QY 448 LSLIALGSRDDIYLSLMLTAKGNL-----NOLQFPFSIHFCITILLHAKKRAIOPFL 501
DB 366 GAVLAFTSERHNLFEKVSITLMAEKGWYVOSOPGSKLGFPRSLHFSVIPGHA--EVDDEL 423
QY 502 KDIRE 506
DB 424 EDMRE 428

Search completed: October 6, 2003, 13:51:28
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173 LHPDIFPGLKIEAIVRIACSLFNGGPDSCGCVTSGGTESILMACKACRDLAFEKGIK - 231


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Db      58 GDDGKLEKVALGSLN-NKDAYGVSGTEANLALRCKINWREKRRG 116
Qy      232 -----TPETVAPQSAHAFAFNKAASYGKIVRPLTKMMEVDVRAARAISR---NTAMI 283
Db      117 LSKNEHPIIIVPTAHFSEKGEEMDLEVIAPRIKEDYTDIDKFKADVEDVYDGIIG 176
Qy      284 VOSTPOFPHGVDPPEVAKLAVKYPILPHVADCLGGLIVEME---KAGYPLEHPDF 339
Db      177 IAGTTEL--GTIDNIEELSKIAKENNIIYHVDAAFGGLVLPFLDXXKKKG--VNYKPDF 232
Qy      340 RVKGVTSISADTHKGYARAKGSSLYLXSKKRYNPFVDTMOGSIYASP-----T 391
Db      233 SL-GVDSITIDPHKMGHCPISGGILFKDIGTKRY--LDVD-----APVLTETROT 281
Qy      392 IAGSRPGISACMAALMHFGENGVEATKQIITKTAFLKSELE--NIKIGFVGNPOTS 449
Db      282 IIGTRVFGGACTYANLRYLRGREGOKRYNECMENLYLXKLENNFPVI---EPILN 338
Qy      450 LIALGSRDF 458
Db      339 IVAIEDEDY 347

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RESULT 2

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DCE_LACLA ID DCE_LACLA STANDARD; PRT; 466 AA.
AC 09CG20; 050645;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15) (GAD).
GN GADB OR LIL290.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OX Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1360;
[1]
RN NCBIN_1360;
RP SEQUENCE FROM N.A., SEQUENCE OF 1-15, AND CHARACTERIZATION.
RC STRAIN-01-7;
RA MEDLINE-99337071; PubMed-10411264;
RA Nomura M., Nakajima I., Fujita Y., Kobayashi M., Kimoto H., Suzuki I.,
  Aso H.;
RT "Lactococcus lactis contains only one glutamate decarboxylase gene.";
RL Microbiology 145:1375-1380(1999).
[2]
RN NCBIN_1360;
RP SEQUENCE FROM N.A.
RC STRAIN-IL1403;
RA MEDLINE-2135186; PubMed-11337471;
RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
  Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
  lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
-1- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
  THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE
  (By similarity).
-1- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
-1- COFACTOR: Pyridoxal phosphate (By similarity).
-1- MISCELLANEOUS: The enzyme is maximally active at pH 4.7. The
  activity is stable at acidic pH values; there is no activity in
  the neutral pH range. At pH 4.1 the enzyme activity is retained
  at temperatures up to 70 degrees Celsius.
-1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
  GAD, HDC AND TYRDC).
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DR EMBL; AB010789; BAA24585.1; -
DR EMBL; AE006361; AAK05388.1; -
DR PIR; B86786; B86786.
DR InterPro; IPR002129; Pyridoxal dec.
DR Pfam; PF00282; pyridoxal dec. 1.
DR PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 466 AA; 53926 MW; BDCD732253E473C2 CRC64;

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Query Match

8 %; Score 261.5; DB 1; Length 466;

Best Local Similarity 23.0%; Pred. No. 7.2e-13; Matches 102; Conservative 76; Mismatches 222; Indels 43; Gaps 13;

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Qy 116 LPSQGLSSAVLEKLEKLEYSMDAFMOEGRASGVYSGEELTE-LVKKAYGFAWNPILH 174
Db 27 LPKRYKLAQOSIERVAVYOLVODMDEGNARLNLAFCQTYMPREAVKLSQLEKNAD 86
Qy 175 PDIFPGLRKIEAIVRIACSLFENGSDS--CGCVTSGTIESIIMA-----CKACRDL 224
Db 87 KSEYPRTEIENKVCNMADIADLNWASERKFMGTSTIGSEACMLGGMANKFSWRKRAEL 146
Qy 225 APEKGIKTPETIYAPQSAHAFAFNKAASYFGKIVRPLTK-MMEVDVRAARAISRNT--- 280
Db 147 GIDINAKKRPVLISSGYQWCEKFCIYWDIEKREYPMDEHMSINLDKMYDVDEYTCV 206
Qy 281 --AMLYCSTPOEPH-GVIDPPEVAKLAVKYPILPHVADCLGGLIVEMKAGYPLEHPF 337
Db 207 VGIMGITVGRDDIKALDNLIEYVKQTDYKHYHVDAAAGSLVAFVEP-----ELSM 261
Qy 338 DFRVAVTSISADTHKGYARAKGSSLYLXSKKRYNPFVDTMOGSIYASPTTASRP 397
Db 262 DFLKNVVISINTSGHYGLVPGVAVLNRDKKYLEEELIFVYSYLGDELPTMAINFHS 321
Qy 398 GGISACMAALMHFGENGVEATKQIITKTAFLKSELENIKIGFVGN--POLSLAL-- 453
Db 322 ASOLIQYTNFVRYGVDGKAIHERTHKAMFLAKTEK-TGFEIIMNGSQLPTVYKYL 380
Qy 454 --GSRDPDIYRLSNMTAKGWNLANLOQPPSI-HECITLILNAR---KRVAIOFLKDR 505
Db 381 KEDSNKGWMLYDLADLMLKMGVPAVPLPKNLNENIIRLVIRADFGNNAFPNYQDMQ 440
Qy 506 ESYTQIMK-----NPKAKTTG 521
Db 441 EAIEALNKAHILYHEEPENKTYG 463

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RESULT 3

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DCE_LACLC ID DCE_LACLC STANDARD; PRT; 466 AA.
AC 030418;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15).
GN GADB.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OX Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
NCBI_TaxID=1359;
[1]
RN NCBIN_1359;
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN-MG1363;
RA MEDLINE-98143417; PubMed-9484886;
RA Sanders J.W., Leenhouts K., Burghoorn J., Brands J.R., Venema G.,
  Kok J.;
RT "A chloride-inducible acid resistance mechanism in Lactococcus lactis
  and its regulation."
RL Mol. Microbiol. 27:299-310(1998).
-1- FUNCTION: CONVERTS INTERNALIZED GLUTAMATE TO GABA AND INCREASES
  THE INTERNAL PH. INVOLVED IN GLUTAMATE-DEPENDENT ACID RESISTANCE.
-1- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
-1- COFACTOR: Pyridoxal phosphate (By similarity).
-1- INDUCTION: EXPRESSION IS HIGHEST AT ONSET OF STATIONARY PHASE IN

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CC PRESENCE OF NACL AND GLUTAMATE, AND AT LOW PH. CHLORIDE-DEPENDENT
 CC EXPRESSION IS ACTIVATED BY GADR.
 CC -1 SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: AF005098; AAC46188.1; -
 DR InterPro: IPR002129; Pyridoxal.dec.
 DR Pfam: PF00282; Pyridoxal.dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 DR Lyase; Decarboxylase; Pyridoxal phosphate.
 FT BINDING 277 277 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 466 AA; 53849 MM; 28894EB3FEEB16BD C64;
 Query Match 8.7%; Score 258.5; DB 1; Length 466;
 Best Local Similarity 22.3%; Pred. No. 1.2e-12;
 Matches 101; Conservative 74; Mismatches 215; Indels 63; Gaps 12;
 QY 116 LPSGLSSAVLEKTEKXSSMDAFMOEGRASGVYSGEKLTE-LTVKAYGDFAMSNPLH 174
 Db 27 LPRKKLAQOSIEPRVAQVLOVDEMLDEGNARLNATFCQTYMEPEAKYKMSQTEKNAID 86
 QY 175 PDIFPGLRKIEAEIVRIACSLFNGGPS--CGCVTSGGTESTILMA-----CKACRDL 224
 Db 87 KSEYPRTEIEINRCVNMADLMANSEKGIYGTSTIGSSSEACMLGAMMKFSWRRAEKL 146
 QY 225 AFEKGITPELVQAQSAHAANKAASYFGMKIVRPLTKMEVDVRRAMRAISRNTAMLV 284
 Db 147 GLDINAKKPNLVISGYOVCEKFCVYWDIEMREVPMD-----REHMSINLEKVM 196
 QY 285 CSTPFPFHGYV-----DVPYEVAKLAVKKKPIHLVDACGGELIVME 327
 Db 197 DYVDERTIGVINGIGITTYGKYDIDKALDNLIEYKNQOTDKYVYIHDAASGGLYAPVE 256
 QY 328 KAGYPLEHPDEFKVGVTISADTHKYGYAPKSSLVLYSDKKYRNTQFVYDPMOGIY 387
 Db 257 P-----ELENDFRLKNVYSINTSGHKYGLVYGVGWLMRDKYLPRELLIKVYSLGEL 311
 QY 388 ASPIIASSRPGISAAACMAALMHGNGYVATQIIKTANFLKSELENIKIVFGN-- 445
 Db 312 PTMAINFSHASQILIGQYNEFVRGFGDYKAIHERTHVAMYLAEIEEK-TGMEIINDG 370
 QY 446 POLSLIAL-----GSRDFIYRLSNLMTAKGMNINLOFPPSI-HFCITLHAR----KR 495
 Db 371 AQLPIVCYKLEKNSRGNLIDLDRLMLKMOVPAVPLPKNLENIQRLVITADGSMN 430
 QY 496 VALQFLKDIRESVTQIMK-----NPKAKTTG 521
 Db 431 MAFNYVODMOEALDALNKAHLFHQEPENKTYG 463
 RESULT 4
 DCEC_LISTIN STANDARD; PRT; 467 AA.
 AC 0928K4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probabl glutamate decarboxylase gamma (EC 4.1.1.15) (GAD-gamma).
 GN L1N2528.
 OS Listeria innocua.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1642;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CLIP.11262 / Serovar 6a;

RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
 RA Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 RA Charbit A., Chetouani F., Couve E., de Daruvar A., Denoux P.,
 RA Domann E., Dominguez-Bernal G., Duchud E., Durant L., Dussurget O.,
 RA Entian K.-D., Fsihl H., Garcia-del Portillo F., Garrido P.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 RA Jones L.-M., Kaerst W., Kneft J., Kuhn M., Kunst F., Kurpkat G.,
 RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjati H.,
 RA Nordstiek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Trieretz A.,
 RA Vazquez-Boland J.-A., Voss H., Wehlund J., Cossart P.,
 RA "Comparative genomics of Listeria species",
 RT Science 294:849-852(2001).
 CC -1 CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
 CC -1 COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1 SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: AL596172; CAC97755.1; -
 DR PIR: AC1748; AC1748.
 DR Listlist: L1N02528; -
 DR InterPro: IPR002129; Pyridoxal.dec.
 DR Pfam: PF00282; Pyridoxal.dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 DR Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
 FT BINDING 278 278 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 467 AA; 53690 MM; 008AB18FEF274590 C64;
 Query Match 8.1%; Score 242; DB 1; Length 467;
 Best Local Similarity 20.4%; Pred. No. 2.4e-11;
 Matches 100; Conservative 92; Mismatches 222; Indels 76; Gaps 15;
 QY 95 TKDISKMSF---LKVDEYKALPSGLSSAVLEKTEKXSSMDAFMOEGRASGV-- 149
 Db 4 SENDKRKHESIRIPLFGSEESTSIPKYLKKEMPERIAQVLYKQDQMDGNARONLAT 63
 QY 150 --YGEKTELVKAYGDFAMSNPLHPIFGRLKIEAEIVRIACSLFNGGPS--CGC 205
 Db 64 FQGYMEKEAEIILM---AETLEKNAIDKSEYQJTAELNRCVNILADLMNPKESYLG 120
 QY 206 VTSGGTESILMACAC---RDLAPEKGI---KTPREVAQSAHAANKAASYFGMKIV 257
 Db 121 STVGSSSEACMLGGLAMKFRMNNNAEKRLDIOARPNLIISSGYOVCEKFCVYWDVNR 180
 QY 258 RVPLTK-MAEVDVRRAMRAISRNTAMLV-----CSTPFPFH-GVIDPPEVAKLAVKKI 310
 Db 181 VVPRDKENLSLDEKVEFLVDERTIGVIGITTYGKFDIALDDEVEAYNEANEHQL 240
 QY 311 PLHVDACIGFLIVFMEKAGYPLEHPDEFKVGVTISADTHKYGYAPKSSLVLYSDK 370
 Db 241 VIHIDGASGAMFTFVNP-----ELPMDFRLKNVYSINTSGHKYGLVYGVGILMKDKE 295
 QY 371 YRNTQFVYDPMOGIYASPIIASSRPGISAAACMAALMHGNGYVATQIIKTANFL 430
 Db 296 YLPKELFEVSYLDGSMPTMAINFSRSASQILIGQYNEFLRGGFGDYRIHERTKRYTAYL 355
 QY 431 KSELENIKIVFGN--POLSLIALGSHD-----FDIYRLSNLMTAKGMNINLOFPPSI 483
 Db 356 SKTYEK-SGYEIIINDSNLPIVCYKLDKDDLDVEMTLYLADQLMKMOVPAVPLP--- 411
 QY 484 HFCITLHARRKRAVLIQFLKDIRESVTQIMKPKAKTTGMAIYMAQTIVDRNNVAELSS 543
 Db 412 -----ADLSDTIIOF-----VCRADLGYNVAEEFAA 438

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OY      544 VFLLSLXSD 553
DB      439 DFADALHMLE 448

RESULT 5
DCEA_ECO57
ID      DCEA_ECO57      STANDARD:      PRT:      466 AA.
AC      P58228;
DT      16-OCT-2001 (Rel. 40, Created)
DT      16-OCT-2001 (Rel. 40, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN      GADA OR GADS OR Z4930 OR ECS4397.
OS      Escherichia coli O157:H7.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=83334;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX      MEDLINE=21074935; PubMed=11206551;
RA      Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA      Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirpatrick H.A.,
RA      Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA      Grodeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA      Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA      Welch R.A., Blattner F.R.;
RT      *Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.;
RL      Nature 409:529-533(2001).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=O157:H7 / RIMD 050952;
RX      MEDLINE=21156231; PubMed=11258796;
RA      Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA      Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA      Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA      Kuhara S., Shiba T., Hattori M., Shingawa H.;
RT      *Complete genome sequence of enterohaemorrhagic Escherichia coli
RT      O157:H7 and genomic comparison with a laboratory strain K-12.*;
RL      DNA Res. 8:11-22(2001).
CC      -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA (BY SIMILARITY).
CC      -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
CC      -1- CORCTOR: Pyridoxal phosphate (By similarity).
CC      -1- SUBUNIT: Homohexamer (By similarity).
CC      -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DPC,
CC      GAD, HDC AND TYRDC).
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL; AE005577; AAG58658.1; -
DR      EMBL; AP002565; BAB37820.1; -
DR      PIR; E91178; E91178.
DR      PIR; F86024; F86024.
DR      InterPro: IPR002129; Pyridoxal_dec.
DR      Pfam: PF00282; pyridoxal_dec; 1.
DR      PROSITE: PS00392; DDC-GAD-HDC_YDC; 1.
KW      Lyase; Decarboxylase; Pyridoxal phosphate; Multigene family;
KW      Complete proteome.
FT      BINDING      276      276      PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ      SEQUENCE      466 AA; 52699 MW; C7F9623DBB24F489 CR664;

Query Match      7.9%; Score 236.5; DB 1; Length 466;
Best Local Similarity      21.8%; Pred. No. 6,6e-11;
Matches      109; Conservative      86; Mismatches      206; Indels      99; Gaps      21;
OY      61 FQPSLMSRFKKKKKRL---TRKMPIIGRKIKDILKIKDDISKMSFLKDKF-YVAKL 116

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DB      9 FNSLDSRFGAIASTIESKRF-----LHEMRDVI---AFQIINDELIDGN 55
OY      117 PSQGLSSSAVLEKLEYSSMDAFWDEGRASGVYSGEKLTELIVKAYDFAFNSNPLHPD 176
DB      56 ARQNLATPC-----QTWDD-----ENVHLMDSIN-----KNWIDME 88
OY      177 IFPGLEKIEAEIVRIACSLF-----NGPDSGCVTSGCTESILMACAC-----RDJ 224
DB      89 EYPOSAIDRLRCVNMVADLMHAPAPKNG--QAVGTWTISSEACMLGMAMKWRMRKRM 146
OY      225 AFEKIKTTEIYAPQSAHAFAFKKASYFGMKIVRVPLTK-MNEVDVRAARRAISRTATL 283
DB      147 AAGKPTKPNLVC-CPVQICMKHFAKRYMDVELEIRPMRGQLFMDKRMIEACDEPTICV 205
OY      284 V-----CSTPQFPGVVIDPVEVAKLWKKIPLVADACGFLITVMEKAGVLEHP 336
DB      206 VPTFGVITGNKNEFPQPLDALDKF-QADTGIDIMHIDMAAGSGLFAFVAP-----DIV 259
OY      337 FDFRKGVNTSISADTHKRYGAPKSSLVLYSDKKYNNYGFVDTDMGGIYASPTIAGSR 396
DB      260 WDFRLPVRKXISASGKFLGAPLPGCGVIMRDEALPQLVFNVDYLGQIGTFAINFSR 319
OY      397 PGGISACGAALMHGNGENVYVATKOITATFLASELNINGIVF---GNPQSLIAB 453
DB      320 PAGQVIAQYEFRLRGREGYTVQNASYQVAAVLADLAKL-GPYEICTGRPDGIPAV 378
OY      454 GSR-----DPDIYLSNIMTAKGNLNLQLOFP-----PSIHFCITLLHARRKRAVIOF 500
DB      379 CERKKEGEPGYTIVLDSFRLNRGM-----QVPATLGEATDIYVMIMKCRGEMDF 433
OY      501 ----LKDIRESVTQIMKNPK 516
DB      434 AELLLEDYKASLKYLSDBPK 453

RESULT 6
DCEA_ECOLI
ID      DCEA_ECOLI      STANDARD:      PRT:      466 AA.
AC      P80063;
DT      01-MAR-1992 (Rel. 21, Created)
DT      01-DEC-1992 (Rel. 24, Last sequence update)
DT      28-FEB-2003 (Rel. 41, Last annotation update)
DE      Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN      GADA OR GADS OR B3517 OR C4328.
OS      Escherichia coli, and
OS      Escherichia coli O6.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Escherichia.
OX      NCBI_TaxID=562; 217992;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12;
RX      MEDLINE=92394884; PubMed=1522060;
RA      Smith D.K., Kassam T., Singh B., Elliott J.F.;
RT      *Escherichia coli has two homologous glutamate decarboxylase genes
RT      that map to distinct loci.*;
RL      J. Bacteriol. 174:5820-5826(1992).
RN      [2]
RP      SEQUENCE AND SEQUENCE OF 148-466 FROM N.A.
RC      STRAIN=ATCC 11246;
RX      MEDLINE=92155241; PubMed=1740158;
RA      Maras B., Sweeney G., Baria D., Bossa F., John R.A.;
RT      *The amino acid sequence of glutamate decarboxylase from Escherichia
RT      coli. Evolutionary relationship between mammalian and bacterial
RT      enzymes.*;
RL      Eur. J. Biochem. 204:93-98(1992).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=K12 / MG1655;
RX      MEDLINE=94316500; PubMed=8041620;
RA      Sofia H.J., Burland V., Daniels D.L., Plunkett G. III, Blattner F.R.;
RT      *Analysis of the Escherichia coli genome. V. DNA sequence of the

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RT region from 76.0 to 81.5 minutes.";
 RL Nucleic Acids Res. 22:2576-2586(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-06.H1 / CF073 / ATCC 700928;
 RX MEDLINE-2238823; PubMed-12471157;
 RA Resch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
 Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
 Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
 RA Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
 RT "Extensive mosaic structure revealed by the complete genome sequence
 of uropathogenic Escherichia coli.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
 RN [5]
 RP SEQUENCE OF 1-22.
 RX MEDLINE-94033862; PubMed-7764225;
 RA Yoshida T., Yamashino T., Ueguchi C., Mizuno T.;
 RT "Expression of the Escherichia coli dimorphic glutamic acid
 decarboxylases is regulated by the nucleoid protein H-NS.";
 RL Blost. Biotechnol. Blochem. 57:1568-1569(1993).
 RN [6]
 RP SEQUENCE OF 382-392.
 RC STRAIN-K12 / EMG2;
 RX MEDLINE-97443975; PubMed-9298646;
 RA Link A.J., Robison K., Church G.M.;
 RT "Comparing the predicted and observed properties of proteins encoded
 in the genome of Escherichia coli K-12.";
 RL Electrophoresis 18:1250-1313(1997).
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA.
 CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- SUBUNIT: Homohexamer.
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 GAD, HDC AND TYRDC).
 CC -1- DATABASE: NAME-Worthington enzyme manual;
 WWW="http://www.worthington-biochem.com/manual/g/GADP.html".
 CC -----
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 CC -----
 DR EMBL: M64024; AAA23833.1; -;
 DR EMBL: X63123; CAA44834.1; -;
 DR EMBL: U00039; AAB18493.1; -;
 DR EMBL: AE000428; AAC76542.1; -;
 DR EMBL: AE016768; AAN82764.1; ALT_INTR.
 DR PIR: S47737; S24234.
 DR ECO2DBASE: D046.5; 6TH EDITION.
 DR ECO2DBASE: E046.5; 6TH EDITION.
 DR EcoGene: EG50009; gada.
 DR InterPro: IPR02129; Pyridoxal dec.
 DR Pfam: PF00282; pyridoxal dec. 1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC. 1.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Multitene family;
 KW Complete proteome.
 FT BINDING 276 PYRIDOXAL PHOSPHATE.
 FT CONFLICT 64 C -> S (IN REF. 2).
 FT CONFLICT 73 H -> R (IN REF. 2).
 FT CONFLICT 153 D -> N (IN REF. 2; AA SEQUENCE).
 FT CONFLICT 165 C -> S (IN REF. 2).
 FT CONFLICT 208 T -> N (IN REF. 2).
 FT CONFLICT 295 L -> V (IN REF. 2).
 FT CONFLICT 355 D -> N (IN REF. 2; AA SEQUENCE).
 SQ SEQUENCE 466 AA; 52685 MW; 86F963E710553E22 CRC64;

Query Match 7.98; Score 236.5; DB 1; Length 466;
 Best Local Similarity 21.88; Pred. No. 6.6e-11;
 Matches 109; Conservative 86; Mismatches 206; Indels 99; Gaps 21;

QY 61 FQPSLMSRKKCKFKL--TRKPIIGRIQDKLNTKDDISKNSFLAYDKE-YVKAL 116
 Db 9 FRSELDLSRFGAKAISTIAESKRFP-----LHEMRDVF-----AFQIINDELYLDGN 55
 QY 117 PSQGLSSAVLEKLEKLEISSMDAFWQGRASGTYVSGEKELTLLVKAAGPAMNPLHPD 176
 Db 56 ARONLAFFC-----QTWDD-----ENYHKMLDLSIN-----KNWIDKE 88
 QY 177 IFPRLRIEAEIVRIACSLF-----NGSPDSCGCVTSGGESILTMCKAC-----RDL 224
 Db 89 EYFQSAIDLRCAVMNVAIDLHAPAPKNG--QAVGTNTIGSSEACGLGMAMKMRKRME 146
 QY 225 AFEGKIPTEIVAPQSAHAFAFNKAASYGKIVVPLTK-MNEYDVAMRAISRNTAML 283
 Db 147 AAGKPTPKPNLYC-GPQIGCMHKARARWDELRIPIRPGOLFMDPRMIEACENTIGV 205
 QY 284 V-----CSTPQFPHGVIDVPEVAVLAKYKIPHLVADCLGGLFLVFMKAGYPLEHP 336
 Db 206 VPTFGVTVTGVEYEPQPLHDLDF--QADYCIDIDMIDAAGSGFLAFVAP-----DIV 259
 QY 337 FDFPRVKVTSISADTHKYGYPARKSSLYLVSDKRYRYQFPVDMDMGGIASPTIAGSR 396
 Db 260 WDFRLPRVKSISASGHFGLAPLGGVYIMDEBALPQELVENVYDLGGQITPAINFSR 319
 QY 397 PGISACMAALMHFGENGVEATKQIITKARFLKSELENIGIFV---GNPOLSLIAL 453
 Db 320 PAGVIAQVYEFPLAGREGTKKVNASTQVAAYLADELAKL-GYEFICIGRPDEGIPAV 378
 QY 454 GSR-----DFDIYRLSNLTAKGMNLQDF-----PSIHFCITLLHARRVAIOF 500
 Db 379 CFKLKDEDEPGTYLTDLSERLRLRGW-----QVPAFTLGGRATDIVWRIMCRGFEWDF 433
 QY 501 ----LKDIRESVQIMKNPK 516
 Db 434 AELLLEDYKASLYLSDHPK 453

RESULT 7
 DCEC_LISMO
 ID DCEC_LISMO STANDARD; PRT; 467 AA.
 AC Q8Y4K4;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probabl glutamate decarboxylase gamma (EC 4.1.1.15) (GAD-gamma).
 GN LMO2434.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-EGD-e / Serovar 1/2a;
 RX MEDLINE-21537279; PubMed-11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
 RA Charbit A., Cherouni F., Couve E., de Darvar A., Deboux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
 RA Entian K.-D., Eschl H., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
 RA Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkat G.,
 RA Madueno E., Maitouram A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlueter T., Simoes N., Trierz A.,
 RA Varquez-Boland J.-A., Voss H., Wehland J., Cozzari P.;
 Science 294:849-852(2001).
 CC -1- Comparative genomics of Listeria species.";
 CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 GAD, HDC AND TYRDC).
 CC -----
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CC EMBL: AL591983; CAD00512.1; -.
 DR PIR: AB1379; AB1379.
 DR Listlist: LMO02434; -.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
 FT BINDING 278 278. PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 467 AA; 53640 MW; 64A8CB6FC82B8CF CRC64;

Query Match 7.9%; Score 234; DB 1; Length 467;
 Best Local Similarity 21.3%; Pred. No. 1e-10;
 Matches 100; Conservative 87; Mismatches 233; Indels 50; Gaps 15;

OY 95 TKDDISKNSF--LKVDEYKALPSQGLSSAVLEKLEYSSMDAFWQGRASGTV-- 149
 DB 4 SEDDKRQESYRIPLFGSEESTSIPKYVLKKEPEPRAYQVLVDQMLDEGNARQNLAT 63
 OY 150 --YSESEKTELVAAYGDFAMSNPLHDPFGKLEAEYRIACSLFNGGPD--CCG 205
 DB 64 FCQTYMEKEAEILM--AETLEKNAIDKSEYQPTAELEKRCVNIADLNNAPKDMSYLGT 120
 OY 206 VMSGGESITLMAKCKC---RDLAPEKGI---KTPETIAPQSAHAFAFKASVFGMKIV 257
 DB 121 STVGSESEACMLGGLMKFRMRNAEKRGIDQAKRPNLISSGYOVCEKFCVYMDVDR 180
 OY 238 RVPPLK-MWEDVRAAMRAISRNTAMLV-----CSTPOEPH-GVIDPPEVAKLAVKYKI 310
 DB 181 VYPMKNNHLSLDVDFVFDLVDYTGIVGIGITGTGKRDIDQLDKEVEAVNETNEHQL 240
 OY 311 PLHYVACGLGFLIVMEKAGYPLEHPDFPRVAGVYSISADTKYGAAPGSSVLVSKK 370
 DB 241 VHIIDGASGAMFTPVNP---ELPMDERLKNVYSISNGHKYGLVYPGVWIMLKDE 295
 OY 371 YHNOYFVDTDMOGGIYASPTIAGSPGIGISAACMAALMHFGENGVEATKQIITAPRL 430
 DB 296 YLPKLEIPEVSYLGGSMPTMAINFSRSQIIGOTYINPLRYFEGYREIHEKTKITAYL 355
 OY 431 KSELENKIGIEVFN--POLSLIALGSR---DFDIYRLSNLMTAKGNLNOLOPPSI 483
 DB 356 AKTVEK-SCGFELIINDGALPIYCYKMKKEGLDVENTLYDLADQLMKGMQVAPYLPADL 414
 OY 484 HECITLLHARK-----RAVIOFLKDIRESV-----TQIMKNPKAKTTGNG 523
 DB 415 SDTIQRFVYCRADLGYNVAEEFADAFDAIHNLHARVLYHDKERNDYSG 464

RESULT 8
 DCE_PETHY STANDARD: PRT: 500 AA.
 ID DCE_PETHY
 AC 007346;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutamate decarboxylase (EC 4.1.1.15) (GAD).
 GN GAD.
 OS Petunia hybrida (Petunia).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiales; Solanales; Solanaceae; Petunia.
 OC NCBI_Taxid=4102;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal;
 RX MEDLINE=93374956; PubMed=8366104;
 RA Baum G., Chen Y., Arazi T., Takatsuji H., Fromm H.;
 RT "A plant glutamate decarboxylase containing a calmodulin binding

RT domain. Cloning, sequence, and functional analysis.";
 RL J. Biol. Chem. 268:19610-19617(1993).
 CC -I- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
 CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
 CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
 CC BIOSYNTHESIS.
 CC -I- CATALYTIC ACTIVITY: L-glutamate + 4-aminobutanoate + CO(2).
 CC -I- COFACTOR: Pyridoxal phosphate.
 CC -I- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
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CC EMBL: L16797; AAA33709.1; -.
 DR EMBL: L16977; AAA33710.1; -.
 DR PIR: A48767; A48767.
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; pyridoxal_dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding.
 FT BINDING 277 277. PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 FT DOMAIN 469 500. CALMODULIN-BINDING.
 SQ SEQUENCE 500 AA; 56726 MW; 72A043CB885AE10D CRC64;

Query Match 7.8%; Score 233; DB 1; Length 500;
 Best Local Similarity 22.6%; Pred. No. 1.4e-10;
 Matches 104; Conservative 82; Mismatches 215; Indels 60; Gaps 15;

OY 92 LNKTT--KDDISKNSFLKVDKEYKA-----LPQGLSSAVLEKLEYSSMDAFWQEG 143
 DB 3 LSKTYSQSVSHSHPA---SKYVRSILPRFKMPDINSIFKEAYQIINDLMDONPRIN 59
 OY 144 RASGTVYSGEKEKTELVAAYGDFAMSNPLHDPFGKLEAEYRIACSLFNG---G 199
 DB 60 LASFTYTWMEPECDKLM---DSINKNVDMDEVPVTEIQRNRCVNMIAHFNAPLEDG 115
 OY 200 PSCGCVYSGTSEITLMAKCKACRDALFE-----KGITPEIYAPQSAHAFAFKA 248
 DB 116 ETAVGAGVYSSSEALMLA---GLAFKRWONKKKAAQKPCDKKNITVYGAOVCEWF 170
 OY 249 ASYFGMKIYRVPLTKMEEV-DVRAAMRAISRNTAMLVGSTPOEPHGVIDPPEVAKLAVK 307
 DB 171 ARYFEVELKEVLSGGYVMDPEKAVEMVDENTICVAALISGLNGEPEDVARKLMDLVE 230
 OY 308 -----YKIPLHVADCLGFLIVMEKAGYPLEHPDFPRVAGVYSISADTKYGAAPGS 361
 DB 231 KKKETGMDFPIHVDAASGFIAPFI---YP-ELEMDERLPLVKSISNGHKYGLVYGI 285
 OY 362 SLVYISDKKYRNYQFVDIDMGGGIYASPTIAGSPGIGISAACMAALMHFGENGVEATK 421
 DB 286 GNVVWRNKDDLDDELIFHINYLGAQDPFTTLNFSKSSGOVLAQYQLRLGEGYKNWE 345
 OY 422 QIITKARFLKSELENKIGF-----VFGNPOSLIALGSRDPIYRLSNLMTAKGNLNO 476
 DB 346 NQENANSVIRELEK-TGFENIISKEIGVPLVAFSLKDRNQRNNEFISITELRRFGIYVA 404
 OY 477 LQPPSIHFCITLLHA-----RKNVAIOFLNDIRESVYQI 511
 DB 405 YMPNNAQH-IVLRAVIREDSRTLAERLVADIEKVLHEL 444

RESULT 9
 DCEB_LISMO STANDARD: PRT: 464 AA.
 ID DCEB_LISMO
 AC 09EYW9; 08Y450; 09AG00;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Glutamate decarboxylase beta (EC 4.1.1.15) (GAD-beta).
 GADB OR LMO2363.
 OS Listeria monocytogenes.
 OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 OX NCBI_TaxID=1639;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LO28 / Serovar 1/2c, and EGD5;
 RX MEDLINE=21206233; PubMed=11309128;
 RA Corder P.D., Gahan C.G.M., Hill C.;
 RT "A glutamate decarboxylase system protects *Listeria monocytogenes* in
 gastric fluid";
 RL Mol. Microbiol. 40:465-475(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EGD-e / Serovar 1/2a;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusnock C., Amend A.,
 Baquero F., Berche P., Bloeker H., Brandt P., Chakraborty T.,
 Charbit A., Chetoui F., Couve E., de Daruvar A., Dehoux P.,
 Doman E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurgeat O.,
 Ertan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
 Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
 Jones L.-M., Kaerst U., Kreft J., Kuhn M., Kunst F., Kurapkhat G.,
 Madueno E., Maitounam A., Mata Vicente J., Ng E., Nedjari H.,
 Nordlek G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
 Remmel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
 Vazquez-Boland J.-A., Voss H., Wenland J., Cossart P.;
 RT Comparative genomics of *Listeria* species.;
 RL Science 294:849-852(2001).
 CC -1- FUNCTION: Converts internalized glutamate to GABA and increases
 the internal pH. Involved in glutamate-dependent acid resistance
 in gastric fluid.
 CC -1- CATALYTIC ACTIVITY: L-glutamate -> 4-aminobutanoate + CO(2).
 CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 GAD, HDC AND TYRDC).
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF309077; AAG22562.1; -;
 DR EMBL: AF329447; AAK17187.1; -;
 DR EMBL: AL591983; CAD00441.1; -;
 DR PIR: AC1370; AC1370.
 DR Listlist: LMO02363; -;
 DR InterPro: IPR002129; Pyridoxal_dec.
 DR Pfam: PF00282; Pyridoxal_dec.1.
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
 KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
 FT BINDING 275 275 A -> P (IN STRAIN LO28).
 FT VARIANT 92 92 E -> D (IN STRAIN LO28).
 FT VARIANT 124 124 E -> D (IN STRAIN LO28).
 FT VARIANT 261 261 F -> L (IN STRAIN EGD5).
 FT VARIANT 375 375 C -> R (IN STRAIN EGD5).
 FT VARIANT 380 381 DD -> TT (IN STRAIN LO28).
 FT SEQUENCE 464 AA; 53542 MW; F2E2778CFD1E2C36 CRC64;
 SQ
 Query Match 7.88; Score 232.5; DB 1; Length 464;
 Best Local Similarity 21.3%; Pred. No. 1.3e-10;
 Matches 103; Conservative 90; Mismatches 212; Indels 79; Gaps 17;
 OY 66 LMSRPFKKCFKLRRKPIIRKIDKNTKDKDISKMSFLYKDKYKALPQGLSSA 125
 DB 2 LYSKKNKESI---LEPVFSSAEDR-----DIPK---YTGKPELEPRIRAYLKDE 47
 OY 126 VLEKLKYSMDAFWQEGRASGTGYSGEKLTELVLKAYGDFAWNSPLHDPFPGLRKIE 185

DB 48 LLDGSAHQRLATFCQ-----TYM-EDBATKLM-----SETLEKNADKSEYPRFALE 95
 OY 186 AEIVRIACSLFNGSPDS--CGCVTSGSTESIL---NACK-ACRDIAFEKI-----KPEI 235
 DB 96 NRCVNITADLWHPKPKDKFQMGSTIGSSSEACMLGMAKFRARAKLGLDIYAKKPNL 155
 OY 236 VAPQSHAAFNKAASYFGKIVRPPLTKMKEVQVRAARRAISNTALVSTPOFPQGI 295
 DB 156 VISSGYOVCKEKCVCYVDDIMRVPMCK-----EKMQLNTDOYLDYDEYTTIGV 205
 OY 296 DPV-----PEVAKLAVK-----YKIPLHVDACGLGFLIVMEKAGVPLEHPD 338
 DB 206 GILGITYGRDYDIALNEKLEENSKTDVKYVIVHDAAGGFTPEVE-----DLIWD 260
 OY 339 FRYKGVTSISADTHKRGYAPKSSLYLVSQKRRNTQFPVDTMOGIVASPTIAGSPG 398
 DB 261 FRUKNVISITSGHKVGLVPGIGVWLMKDESLPEELIFKVSYLGGEMFTMOINFPSRA 320
 OY 399 GISACGAALMHGNGEVYATKQIIRKARFLKSELENIGIFVFGN-PQLSIALGSRD 457
 DB 321 SHIIGQYNNFLRGFECSRTIHOITSDVAQYLAHAYQOTGFDFIINDGSHLPYCYRKLK 380
 OY 458 -----FDYRLSLMLTKAGNNLNOLOPPPSIHFCITLLHARK-----RVAIOFLKDIRES 507
 DB 381 DAVNMTLYDLADRLQRMGQVPAYPLPKSLENIITIGRYCRAIDLGFMAEEFIQDROAS 440
 OY 508 VTQI 511
 DB 441 IOEL 444
 RESULT 10
 DCEL_ARATH STANDARD; PRT; 502 AA.
 AC 042521; Q9FPH9;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Glutamate decarboxylase 1 (EC 4.1.1.15) (GAD 1).
 GN GAD1 OR GDH1 OR GAD OR AT5G17330 OR MKP11.30 OR MKP11.18.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=95334488; PubMed=7610159;
 RA Arai T., Baum G., Snedden W.A., Sheld B.J., Fromm H.;
 RT "Molecular and biochemical analysis of calmodulin interactions with
 the calmodulin-binding domain of plant glutamate decarboxylase";
 RL Plant Physiol. 108:551-561(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97471969; PubMed=9330910;
 RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
 Miyajima N., Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
 features of the 1.6 Mb regions covered by twenty physically assigned
 P1 clones";
 RL DNA Res. 4:215-230(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Arabidopsis full length cDNA clones (RAFLs) sequenced by the
 SSP consortium (Saik/Stanford/PGEC)";
 RL submitted (Apr-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
 IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY

RA Yoshida T., Ueguchi C., Yamada H., Mizuno T.;
 RT Function of the Escherichia coli nucleoid protein, H-NS: molecular
 RT analysis of a subset of proteins whose expression is enhanced in a
 RT hns deletion mutant.";
 RL Mol. Gen. Genet. 237:113-122(1993).
 RN [8]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.flexneri; STRAIN=301 / Serotype 2a;
 RX MEDLINE=22272406; Pubmed=12384590;
 RA Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
 RA Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
 RA Sun L., Xue Y., Zhao Y., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
 RA Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
 RA Yu J.;
 RT "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
 RT through comparison with genomes of Escherichia coli K12 and O157.";
 RL Nucleic Acids Res. 30:4432-4441(2002).
 CC - FUNCTION: CATALYZES THE PRODUCTION OF GABA.
 CC - CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
 CC - COFACTOR: Pyridoxal phosphate.
 CC - SUBUNIT: Homohexamer.
 CC - SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
 CC GAD, HDC AND TYRDC).
 CC -----
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 CC -----
 DR EMBL: M84025; AAA23834.1; -;
 DR EMBL: AE000246; AAC74566.1; -;
 DR EMBL: D90791; BAA15163.1; -;
 DR EMBL: D90790; BAA15171.1; -;
 DR EMBL: AE005356; AAG56275.1; -;
 DR EMBL: AP002557; BAB35521.1; -;
 DR EMBL: X71917; CAA50736.1; ALT_SRO.
 DR EMBL: AE015194; AAA43309.1; ALT_INTR.
 DR PIR: B43332; B43332.
 DR PIR: B90891; B90891.
 DR PIR: G85726; G85726.
 DR ECGene: EGI1490; gadB.
 DR InterPro: IPR002129; Pyridoxal dec.
 DR Pfam: PF00282; Pyridoxal dec. 1
 DR PROSITE: PS00392; DDC_GAD_HDC_YDC. 1.
 DR Lyase: Decarboxylase; Pyridoxal phosphate; Multigene family;
 KW Complete proteome.
 FT BINDING 276 276 PYRIDOXAL PHOSPHATE.
 SO SEQUENCE 466 AA; 52668 MW; 8E65330A3C5BAED CRC64;
 Query Match 7.7%; Score 229.5; DB 1; Length 466;
 Best Local Similarity 21.9%; Pred. No. 2.3e-10;
 Matches 108; Conservative 84; Mismatches 209; Indels 93; Gaps 20;
 OY 64 ESIWSRKKKCFKLTIRKPIIGRKIODKLNKTKODISKNNKSPKLVKDE-VYKALPQSGLS 122
 DB 12 ELDSRRGAK-----SITIAESKRPRLEHMRDV---AFQINDELTLIDGNARONLA 61
 OY 123 SSAVLEKLEKSYSSMDAFWQEGRASGVYVSGEKLTELLVAYAGDFANSPLDHPIDFGLR 182
 DB 62 TFC-----QWMD-----ENVHKLMDLSIN-----KNMIDKEEYQSA 94
 OY 183 KIRAEIVIRACSLF-----NGPDSGCGVTSGETSITLACACAC-----RDIAFEKGI 230
 DB 95 AIDLRCAVADLMHAPAKNG--QAVGTNTIGSSSECMGMAKMRMRKREAAGKPT 152
 OY 231 KPEIYVAPSAHAFAFNKAASYFGKIVRPLTK-MMVDVVRAMRAISRNTAMLY----- 284
 DB 153 DKRNLCV-GPVQICMNFARKYMDLEIRTPMRQGLQMDKRMLEACDENTIGVPTFGV 211
 OY 285 -CSTPQPHGVIDPVPEVAKLAVKYKIRPLHVDACLGFLVPEKAGYPLEHFDPRVK 342

DB 212 TYTGNVEFPQPLHDALDKF-QADTGIDIMHIDAASGFLAFVAP-----DIWDRRLP 265
 OY 343 GYVISAADTHKYGKAPGSSLYLSDKKRYNOFFVTDMOGGIYASPTIAGSPGISA 402
 DB 266 RVKISASAGHKFGIAPGCGVWIRDEALPOELVFVWDVAGGICGFALNFSRPAQVI 325
 OY 403 ACNAAALHFGENGVEATKQIKTARFLKSELENKIGIWFV---GNPOLSLALGSR--- 456
 DB 326 AQYEFRLRGREGYTKQNASYQVAAVLADEIAKL-GPYEFICTGRPDEGIPACVFKLD 384
 OY 457 ----DPIYRLSNIMTAKGNLNOLOPP-----PSIHFCITLLHARRVAIOP-----LK 502
 DB 385 GEDPGYTLVDSERLRLRGW-----QVPATLGEANDIYVMRCRGFEMDPALLLE 439
 OY 503 DIRSVYQIKNPK 516
 DB 440 DYKASLYLSDHPK 453
 RESULT 12
 DCE2_ATHH STANDARD; PRT; 494 AA.
 ID DCE2_ATHH
 AC 042472;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 28-FEB-2003 (Rel. 41, last annotation update)
 DE Glutamate decarboxylase 2 (EC 4.1.1.15) (GAD 2).
 GN GAD2 OR GDH2 OR ATIG65960 OR F12P19.12.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98363649; Pubmed=9700069;
 RA Zik M., Arazi T., Snedden W.A., Fromm H.;
 RT "Two isoforms of glutamate decarboxylase in Arabidopsis are regulated
 RT by calcium/calmodulin and differ in organ distribution.";
 RL Plant Mol. Biol. 37:967-975(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=97267149; Pubmed=9112779;
 RA Turano F.J., Thakkar S.S., Fang T., Weisemann J.M.;
 RT "Characterization and expression of NAD(H)-dependent glutamate
 RT decarboxylase genes in Arabidopsis.";
 RL Plant Physiol. 113:1329-1341(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=21016719; Pubmed=11130712;
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
 RA White O., Alonso J., Altieri H., Araujo R., Bowman C.L., Brooks S.Y.,
 RA Buhrer E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,
 RA Dunn P., Etlg P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan C.D.,
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Matli R., Matzball A.,
 RA Miltcher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,
 RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
 RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 408:816-820(2000).

CC -1- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
CC BIOSYNTHESIS (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate.
CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).
CC -----
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CC -----
DR EMBL: U49937; AAC31617.1; -
DR EMBL: U46665; AAC33485.1; -
DR EMBL: AC009513; AAF06056.1; -
DR PIR: H96683; H96683.
DR InterPro: IPR002129; Pyridoxal dec.
DR Pfam: PF00282; Pyridoxal dec. 1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Calmodulin-binding;
KM Multigene family.
FT BINDING 276 276 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
FT DOMAIN 461 494 CALMODULIN-BINDING (BY SIMILARITY).
SQ SEQUENCE 494 AA: 56140 MW: 741E83A25DCBC48C CRC64:

Query Match 7.6%; Score 226; DB 1; Length 494;
Best Local Similarity 23.0%; Pred. No. 4.8e-10;
Matches 93; Conservative 72; Mismatches 192; Indels 48; Gaps 13;

QY 171 NPLHDPIDPGRKIEAIVRIACSLFNG-----GPDSCGVNCGESTILMACKACRDIAF 226
DB 82 NYVMDERPVTTTELQRCVNIARLFENAPLESESTAVGVGSSEATMLA-----GLAF 136
QY 227 E-----KGITPEIYAPOSAHNAFAKASYFGMKIVRYPLTK-----MMEVDVRA 272
DB 137 KRKMOKRKAKGKPRDKPNITVGANVOYCWMEKFAFYFVELKEVNLSEGYVMDDKA- 195
QY 273 KRAISRNTAMLCVSTPQEPFGVYIDPVPEVAKLAVK-----YKIPLHVADCLGGLIYFM 326
DB 196 -EMVDENTICVAAILGSTLNGEFEDYKRLNDLVYKNEETGWNTPIHVDAASGCFIAEFI 254
QY 327 EKAGYPLHPDERFKGVTSISADTHKKYGAAPKSSVLXSDKKRYNQFVDTDMOGI 386
DB 255 -----1P-ELEWDFRLPLVKSINVSCHKYGLVYAGVWVRAAEDLPELLIFHNYLGAD 309
QY 387 YASPTIAGSRPGISAAACMAALMHGNGVYEATKOITKTARFLKSELENIGIFVGNP 446
DB 310 QPTFLNLSKGSQSIQIAYQILIRGFEQYKVMNCLENNVYLKGEIEKTERFIVSKD 369
QY 447 Q-LSLIAAGSRDFD---YRLSNLTAKGMNLNOLQPPPSIHFCITLLHA-----RRRV 496
DB 370 QGVPAVASLKDHSFNEFEISEMLRREGWIVPATYMPADAQH-ITVIRVAVIREDFSR 428
QY 497 AIOPLKDIRESYTOIMKNPKAKTGMGAIYAMAQTTVRNVAEL 541
DB 429 AERLVADISKVHLDELTPSKISKMG-IEGIAENVKERKMEKET 472

RESULT 13
DEB_LISIN
ID DEB_LISIN STANDARD: PRT: 464 AA.
AC Q928R: 28-FEB-2003 (rel. 41, Created)
DT 28-FEB-2003 (rel. 41, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Glutamate decarboxylase beta (EC 4.1.1.15) (GAD-beta).
GN GADB OR LIN2463.
OS Listeria innocua.

OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_Taxid=1642;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN-CLIP 11262 / Serovar 6a:
RX MEDLINE-21537279; PubMed-11679669;
RA Glaeser P., Frangeul L., Buchrieser C., Rusnlok C., Amend A.,
RA Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
RA Charbit A., Cheuouat F., Couve E., de Darvar A., Dehoux P.,
RA Domene E., Dominguez-Bernal G., Duchaud E., Durant L., Dussauget O.,
RA Entlan K.-D., Fshih H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Haut J., Jackson D.,
RA Jones L.-M., Kaerst U., Kunz M., Kunst F., Kurapkak G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
RA Nordisk G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
RA Remmel B., Rose M., Schueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- FUNCTION: Converts internalized glutamate to GABA and increases
CC the internal pH. Involved in glutamate-dependent acid resistance
CC in gastric fluid (By similarity).
CC -1- CATALYTIC ACTIVITY: L-glutamate - 4-aminobutanoate + CO(2).
CC -1- COFACTOR: Pyridoxal phosphate (By similarity).
CC -1- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).
CC -----
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CC or send an email to license@sib-sib.ch)
CC -----
DR EMBL: AL596172; CAC97690.1; -
DR PIR: AB1740; AB1740.
DR ListList: LIND2463; -
DR InterPro: IPR002129; Pyridoxal dec.
DR Pfam: PF00282; Pyridoxal dec. 1.
DR PROSITE: PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.
KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 275 275 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
SQ SEQUENCE 464 AA: 53599 MW: 4C35CD1395ADE481 CRC64:

Query Match 7.4%; Score 220.5; DB 1; Length 464;
Best Local Similarity 21.2%; Pred. No. 1.2e-09;
Matches 103; Conservative 90; Mismatches 211; Indels 81; Gaps 18;

QY 66 LMSRPKRCFKLTRKMPITGRKIDKLTKTDISKNSFLKVDKEYKALPSGLSSA 125
DB 2 LYSKRNKESY-----LEPVFGSAEDR-----DIPK-----YLAKEPLEPRIAYLVKDE 47
QY 126 VLEKKEYSMDAFQEOGRASCTVYSGEKLTELLVYKAGPFAWNPPLHPIPLKRIE 185
DB 48 LDEGSARONLATTFCQ-----TYM-EDEAKLM-----SELEKNAIDKSEYPTABLE 95
QY 186 AEIVYIACSLFENGSPDS---CGCVTSGTGESITL---MACK-ACRDIAFEKGI---KTPBI 235
DB 96 NRCVNIITDLMHAPDQKFMGTSTIGSSBACMLGMAKFAWKRKAELGLDIYAKRNL 155
QY 236 VAPQSAHAAFNKAASYFGMKIVRYPLTKMMEVDVRAARRAISRNTAMLCVSTPQEPHCVI 295
DB 156 VISSGYCWMEKFCYVWIDMKVYPMK-----DHQMLNTDQVLDVYDEVYIGIV 205
QY 296 DPV-----PEVAKLAVK-----YKIPLHVADCLGGLIYVEKAGYPLEHPFD 338
DB 206 GILGITTYGRYDDIALALEKLEEVNSKTDYKYIHVDAASGFFPPEP-----DIWMD 260
QY 339 FRVKGVTSLADTHYVYGAAPKSSVLVLSDDKRYRYQFVDPDMOGIYASPTIAGSRG 398
DB 261 FRKLVNISINISGKHYGLVYRGIVLWMLKDESYLPELLIFKVSYLGGEMPTQINFSRSA 320

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OY 399 GISAACMAALMHGNGCYEATKOITKTAFLKSELENIGIFVGN--POLSLIALGSR 456
DB 321 SHIIQYNNFLRYGRFRTIHOQTSDVQYLAHVAHQ--TGFDIYNDGSHLPYCYKXK 379
OY 457 D-----FDIYRLSNLMTAKGMNLOQPPSHIFCTILHAKK-----RAVIGFLAKIRE 506
DB 380 DDANVKMTLVLADRLQRMGMQVAPYPLPKNLNIIIOYRVCRADLGFNNAEETIDFOQA 439
OY 507 SVTQI 511
DB 440 SIQEL 444

RESULT 14
DCEA_LYSMO STANDARD; PRT; 462 AA.
AC 09F5P3; 08Y9S6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase alpha (EC 4.1.1.15) (GAD-alpha).
GN GADA OR LMO00447.
OS Listeria monocytogenes.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1639;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LO28 / Serovar 1/2c;
RX MEDLINE=21206233; PubMed=11309128;
RA Colter P.D., Gahan C.G.M., Hill C.;
RT "A glutamate decarboxylase system protects Listeria monocytogenes in
   gastric fluid.";
RL MOL. Microbiol. 40:465-475(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BGD-e / Serovar 1/2a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
   Baquero F., Berche P., Bloecher H., Brandt P., Chakraborty T.,
   Charbit A., Cheouani F., Couve E., de Darvar A., Denoux P.,
   Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
   Entlan K.-D., Fsihi H., Garcia-del Portillo F., Garrido P.,
   Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
   Jones L.-M., Kaerst U., Krefit J., Kuhn M., Kunst F., Kurapkat G.,
   Madueno E., Maitounam A., Mata Vicente J., No E., Nedjari H.,
   Nordstok G., Novella S., de Pablos B., Perez-Diaz J.-C., Purcell R.,
   Rammel B., Rose M., Schlueter T., Simoes N., Tierrez A.,
   Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RT "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -I- FUNCTION: Converts internalized glutamate to GABA and increases
   the internal pH. Involved in glutamate-dependent acid resistance
   in gastric fluid.
CC -I- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -I- COFACTOR: Pyridoxal phosphate (By similarity).
CC -I- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
   GAD, HDC AND TYRDC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF09076; AAG22560.1; -
CC EMBL; AL591975; CAC98526.1; -
CC PIR; AH1130; AH1130.
CC L1stlist; LMO00447; -
CC InterPro; IPR002129; Pyridoxal_dec.
CC Pfam; PF00282; pyridoxal_dec.1.
CC PROSITE; PS00392; DDC_GAD_HDC_YDC; FALSE_NEG.

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KW Lyase; Decarboxylase; Pyridoxal phosphate; Complete proteome.
FT BINDING 273 PYRIDOXAL PHOSPHATE (By similarity).
FT CONFLICT 152 152 S->N (in Ref. 1).
SQ SEQUENCE 462 AA; 52498 MM; EALAA423EEICEZRA CRC64;

Query Match 7.38; Score 218.5; DB 1; Length 462;
Best Local Similarity 20.6%; Pred. No. 1,7e-09;
Matches 97; Conservative 82; Mismatches 210; Indels 83; Gaps 16;

OY 91 KLNKTKDKDISKMSFLAVDKDEYKALPSQGLSSSAVLEKLEYSMAFMEGRASGVY 150
DB 3 KTVNEQNNVPVGFSE-----ESGDLPEKRNKESVDPRIAYQLVKQLIDEGSAROLA 57
OY 151 S-----GEELTELLVAKAYGDFAMSNPLHPDIPGRLKAEIVRIACSLFNGCPD 201
DB 58 TFCQTYMEPEAEQJMAETMEK-----NAIDSEFPQTKLESSCVNMLADIWNDES 109
OY 202 S--CGVTSGETSILMACRAC---RDALFEKGI---KTPETVAPQSAHAFNKAASY 251
DB 110 EHYWGSTVGSSEACMLGGMAMKFRWRSALKNGLDIAKKPSLVISSGYQVCEKFCVY 169
OY 252 FGAKIVNPLTKMNEVDVRRARRAISRNTAMLCSTQFPHGVY-----DVPPE 300
DB 170 WDIELREVPMSE-----EHLSTNTDIDMYVEYTIIGVIGITGTYGKFDIMT 219
OY 301 VAKLAVKY-----KIPLHDAACLGFLIVFMERAGVPLEHPDFRYKGVTSISADTHKY 354
DB 220 LNDLVEDYNNTHDNEVIVHDGASGAMFTPEVEG---LE--WDFRLPNVYSINTSGHKY 274
OY 355 GYAFKGSLLVYSDKRYRNYQFVDTMOGIVASPTIAGSRPGISAAACMAALMHGEN 414
DB 275 GLVYPGVGWLIMRDKEXLEPELVPDVSYLGGHMTPTMAMNFSRSASQITGGYNNFLRFGYE 334
OY 415 GYEATKOITKTAFLKSELENT---KGIVFNG--POLSLIALGSD-----FDIYRLS 464
DB 335 GY---QIHMRTDGAQLQSAVAETGFEIYNDGANLPVCKLDDANVAANTLYDLA 390
OY 465 NLMTAKGMNLOQPPSHIFCTILHA-----RKRAVIOPLKDIRSVTOI 511
DB 391 DRLQMGQVAPYPLPKMKNTTIIOYRVCRADLGFNNAEETIDFOQA 442

RESULT 15
DCE_LYCSES STANDARD; PRT; 502 AA.
AC P54767;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glutamate decarboxylase (EC 4.1.1.15) (GAD) (ERT D1).
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Alisa Craig; TISSUE=pericarp;
RX MEDLINE=95284363; PubMed=7766895;
RA Gallego P.P., Whotton L., Picton S., Grierson D., Gray J.E.;
RT "A role for glutamate decarboxylase during tomato ripening: the
RT characterisation of a cDNA encoding a putative glutamate
RT decarboxylase with a calmodulin-binding site.";
RL Plant Mol. Biol. 27:1143-1151(1995).
CC -I- FUNCTION: CATALYZES THE PRODUCTION OF GABA. THE CALMODULIN-BINDING
CC IS CALCIUM-DEPENDENT AND IT IS PROPOSED THAT THIS MAY, DIRECTLY
CC OR INDIRECTLY, FORM A CALCIUM REGULATED CONTROL OF GABA
CC BIOSYNTHESIS (By similarity).
CC -I- CATALYTIC ACTIVITY: L-glutamate = 4-aminobutanoate + CO(2).
CC -I- COFACTOR: Pyridoxal phosphate.
CC -I- SIMILARITY: BELONGS TO THE GROUP II DECARBOXYLASE FAMILY (DDC,
CC GAD, HDC AND TYRDC).

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 6, 2003, 13:49:49 ; Search time 29 Seconds
(without alignments)
1883.580 Million cell updates/sec

Title: US-10-053-510-8
Perfect score: 2977
Sequence: 1 MPSTDLMLKAFEPYLEILE.....LYSTDVTYQSGMNGSPKPH 568

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 9616862 residues
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES:

Result No.	Score	Query Match	Length	DB ID	Description
1	2553	85.8	568	2	JC5923 sphingosine-1-phos
2	1082	36.3	552	2	T33760 sphingosine-1-phos
3	1069	35.9	544	2	C86405 probable sphingosi
4	1008	33.9	542	2	T29835 sphingosine-1-phos
5	1007.5	33.8	589	2	S70123 sphingosine-1-phos
6	669	22.5	488	2	B69415 group II decarboxy
7	621.5	20.9	414	2	G69536 group II decarboxy
8	567.5	19.1	454	2	G72452 probable glutamate
9	549.5	18.5	473	2	G72753 hypothetical prote
10	518.5	17.4	383	2	D71084 hypothetical prote
11	514.5	17.3	384	2	G75102 group II decarboxy
12	482	16.2	363	2	E69015 glutamate decarbox
13	380	12.8	367	2	C69500 group II decarboxy
14	369.5	12.4	396	2	B64306 hypothetical prote
15	308.5	10.4	355	2	D84192 glutamate decarbox
16	261.5	8.8	466	2	B86786 glutamate decarbox
17	253.5	8.5	460	2	F70975 probable glutamate
18	242	8.1	467	2	AC1378 glutamate decarbox
19	239.5	8.0	304	2	AE3623 glutamate decarbox
20	236.5	7.9	466	1	S24234 glutamate decarbox
21	236.5	7.9	466	2	E91178 glutamate decarbox
22	236.5	7.9	466	2	F86024 glutamate decarbox
23	234	7.9	467	2	AB1379 glutamate decarbox
24	233	7.8	500	2	A48767 glutamate decarbox
25	232.5	7.8	464	2	AC1375 glutamate decarbox
26	230.5	7.7	514	2	TC9315 glutamate decarbox
27	229.5	7.7	466	1	B43332 glutamate decarbox
28	229.5	7.7	466	2	B90891 glutamate decarbox
29	229.5	7.7	466	2	G85726 glutamate decarbox

30	229.5	7.7	520	2	T49478 probable glutamate
31	228.5	7.7	496	2	T01962 glutamate decarbox
32	226	7.6	494	2	H96683 hypothetical prote
33	220.5	7.4	464	2	AB1740 glutamate decarbox
34	218.5	7.3	462	2	AB1130 glutamate decarbox
35	217.5	7.3	467	2	S75150 glutamate decarbox
36	214	7.2	475	2	T36342 probable glutamate
37	209	7.0	502	2	S56177 probable glutamate
38	204	6.9	362	2	D72734 probable histidine
39	202	6.8	500	2	G84431 probable glutamate
40	201.5	6.8	585	2	S53072 glutamate decarbox
41	198	6.7	493	2	H84431 probable glutamate
42	178	6.0	490	2	T44576 L-2,4-diaminobutyr
43	178	6.0	511	2	C58800 L-2,4-diaminobutyr
44	178	6.0	538	2	AB1856 L-2,4-diaminobutyr
45	175.5	5.9	508	2	G83977 L-2,4-diaminobutyr

ALIGNMENTS

RESULT 1
JC5923
sphingosine-1-phosphate lyase (EC 4.-.-) [validated] - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1998 #sequence_revision 08-May-1998 #text_change 17-Mar-2000
C:Accession: JC5923
R:zhou, J.; Saba, J.D.
Biochem. Biophys. Res. Commun. 242, 502-507, 1998
A:Title: Identification of the first mammalian sphingosine phosphate lyase gene and 1
A:Reference number: JC5923; M0ID:98125521; PMID:9464245
A:Accession: JC5923
A:Molecule type: mRNA
A:Residues: 1568 <20>
A:Cross-references: GB:AF036894; NID:92906010; PIND:AAC03768.1; PID:92906011
C:Comment: This enzyme catalyzes the breakdown of sphingosine-1-phosphate which parti
C:Genetics:
A:Gene: spl
C:Superfamily: sphingosine-1-phosphate lyase
C:Keywords: lyase
F:42-60/Domain: Transmembrane #status predicted <TMM>

Query Match 85.8%; Score 2553; DB 2; Length 568;
Best Local Similarity 84.1%; Pred. No. 1.8e-191;
Matches 477; Conservative 43; Mismatches 47; Indels 0; Gaps 0;

QY	1	MPSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPQMQLAMSVVMTLLVWGVEFV	60
DB	1	MPSTDLMLKAFEPYLEILEVYSTKAKNVNGHCTYEPQMQLAMSVVMTLLVWYELI	60
QY	61	FOPESLMSRPKKCKEFLTRKMPITIGRKIDKLKTRDDISKNSPLKVDKVEYKALPSSG	120
DB	61	FOPESLMSRPKKCKEFLTRKMPITIGRKIDKLKTRDDISKNSPLKVDKVEYKALPSSG	120
QY	121	LSSSAVLEKLKEXSSMDAFOEGRASGTYVSGEKLTELTLVKAAYGDFANSLPPIFQ	180
DB	121	MGTAELVLERKESSMDGSGOEKAGAVYNGEPKLTBELVQAYGDFANSLPPIFQ	180
QY	181	LKRIEAIYRIACSLFNGGPDSCGVYSGTESILMACACRDLAFKGIKPEIYAPOS	240
DB	181	LKRIEAIYRIACSLFNGGPDSCGVYSGTESILMACACRDLAFKGIKPEIYAPOS	240
QY	241	AHAFAFKAAHYFEMKIVRPLTGMVMDVDRAMRAISRNTAMLVCTPDPHGVDPVE	300
DB	241	AHAFAFKAAHYFEMKIVRPLTGMVMDVDRAMRAISRNTAMLVCTPDPHGVDPVE	300
QY	301	VAKLAVKRIPLHVDACLGFLIVFMEKAGYPLEHFPDFRVKCVTSISADTHKYYGAPK	360
DB	301	VAKLAVKRIPLHVDACLGFLIVFMEKAGYPLEHFPDFRVKCVTSISADTHKYYGAPK	360
QY	361	SSVLVSDKKYRYNPFVDJDMOGGIIYASPTIAGSRPGISACMAALMHFGENGVEAT	420
DB	361	SSVVMYSNKKRYRYNPFVDJDMOGGIIYASPTIAGSRPGIIACMAALMHFGENGVEAT	420

Db 543 QY 544

RESULT 4

T29835

sphingosine-1-phosphate lyase (EC 4.-.-) B0222.4 [similarity] - *Caenorhabditis elegans*C:Species: *Caenorhabditis elegans*

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 17-Mar-2000

C:Accession: T29835

R:Du, Z.; Gattung, S.

submitted to the EMBL Data Library, February 1996

A:Description: The sequence of *C. elegans* cosmid B0222.

A:Reference number: 220696

A:Accession: T29835

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-542 <DUZ>

A:Cross-references: EMBL:U50312; PIDN:AAA92321.1; CESP:B0222.4

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CESP:B0222.4

A:Introns: 50/71: 74/3: 223/2: 468/2

C:Superfamily: sphingosine-1-phosphate lyase

C:Keywords: lyase

Query Match 33.9%; Score 1008; DB 2; Length 542;

Best Local Similarity 38.1%; Pred. No. 1e-70;

Matches 206; Conservative 121; Mismatches 201; Indels 12; Gaps 7;

QY 19 LEVYSTRKANVNGHCTKPEWQLAMSVVTLIVGYEYVQPELSMRKCKEKL 78

Db 5 LEQYHS-AKDLLEFELRKNPIVLSSTIVATVTLNLRHMLDENGIRKRLSTWETTV 63

QY 79 RKMPITGRIQDKLNTKDISKMSFLKVDKYVALPSSGSSSAVLEKLEYSMDA 138

Db 64 KRPEFRKMDIKQLNVEKLEKSLRIYRSTETFTIPSHSVGRTEVLAAYDDLEG 123

QY 139 -FMQGRASGTVYSGEKL--TELLKAYGDFAMSNPLHPIPGRLKIAEIVRIACSL 195

Db 124 PAFLEBRVSGAVNRRDDDEREMVEYVCKFQWTPMLPKLFPGVRIHAEVYRMCNM 183

QY 196 PNGSPSCCVTSYGSTESILMACACRDIAFEKGIPTPEIAPASAHAAFNKAASYFGMK 255

Db 184 MNDSETCGTMSGSGISILLACLAHRNRLRKGEKYTEWIVPSVHAHAFKAECPRIK 243

QY 256 IYVAVPLTKM-MEVDVAMKRAISRNTAMLVCSFPPRHGVIDVPEYAKIAVYKIPLV 314

Db 244 VKRIPVDPVTEKVDLKKMAALNKRKTCMLVGSAPNPEFGVDDIEAIGOLEYDIPVHV 303

QY 315 DACLGGLIVFMKAGYPLEHPDFRVKGVTSISADTHKKYGAAPKSSSLVLYSDKKYRNY 374

Db 304 DACLGGLFLPLEED---EIRYDFRPGVSSISADSHKGLAPKSSSVLYLNKELHN 359

QY 375 QRFVDTMOGGIYASPTIAGSRPGGISAAACMAALMHGNGEYVETAKOIKTARFLKSEL 434

Db 360 QYFCADMDWGGIYASPTIAGSRPGGISAAACMAALMHGNGEYVETAKOIKTARFLKSEL 419

QY 435 ENIKGIFVGNPQLSLIALGSRD-FDIYRLSNLMTAKGWNLOLPPSIHFCITLLHAR 493

Db 420 SNIKGKILQSPSPVCLVSWTNDGVELYRFHNFMRKEHMOLOLPPAGHIVATNMHTH 479

QY 494 KRYAIOFLDIRSVTQIM--KNPKAKTTGMAIYMAQTVVDRNMVAELSLVFLDSLVS 551

Db 480 PGAAEFVADCRRAAEVFKSHKPSSEDKTSEAIYGLAOSIPRSLVHERFAHAYIDAVYA 539

RESULT 5

S70123

sphingosine-1-phosphate lyase (EC 4.-.-) [similarity] - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: hypothetical protein D9819.5

C:Species: *Saccharomyces cerevisiae*

C:Date: 24-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 19-Apr-2002

C:Accession: S70123

R:Fulton, L.

submitted to the EMBL Data Library, May 1996

A:Description: The sequence of *S. cerevisiae* cosmid 9819.

A:Reference number: S70114

A:Accession: S70123

A:Molecule type: DNA

A:Residues: 1-589 <FUL>

A:Cross-references: EMBL:U51031; NID:g1332635; PIDN:AAB64470.1; PID:g1230658; GSPDB:G

C:Genetics:

A:Gene: SGD:DP1; MIPS:YDR294C

A:Cross-references: SGD:S0002702

A:Map position: 4R

C:Superfamily: sphingosine-1-phosphate lyase

C:Keywords: lyase; transmembrane protein

F:60-72/Domain: transmembrane #status predicted <TM>

Query Match 33.8%; Score 1007.5; DB 2; Length 589;

Best Local Similarity 39.1%; Pred. No. 1.2e-70;

Matches 209; Conservative 108; Mismatches 185; Indels 33; Gaps 12;

QY 51 LLIVWGYE-----VQPESL-----SRKKKCKFKTRKMPITGRIQDKLNTK 97

Db 60 LEVIFCYKILSNFYLKTVGPVRLAVRYEHSRRLEFLRLDSPFLGTVEKVKVKQ 119

QY 98 DISKNSFLVDKKEYV--ALPSGGLSSAVLEKLEYSMDA--DAFMQGRASGTVYSGE 153

Db 120 SIDEL--IRSDQLNMFQPLPSNGIPDQVDEIKLNLDLHHTQKBEKVGAYHGG 177

QY 154 EKITELLVKAIGDFAMSNPLHPIPGRLKIEAIVRIACSLFNGSPDS--CGCVTSGTE 212

Db 178 DDLIHQTAYEYCVANQLPVPFAVRKMESEVSMVLMFNASDTCGTTSGTE 237

QY 213 SIMACKACRDIAF-EKGIPTPEIAPASAHAAFNKAASYFGKIYAVPL--TKMEYDVR 270

Db 238 SILLACISAKMVLNHRGITEPELIAVTAHAFDAAYYFKGLRVELDPTTYQVDLG 297

QY 271 AMRAISRNTAMLVCSFPPRHGVIDVPEYAKIAVYKIPLVNADCLGFLIVFMKAG 330

Db 298 KYVKFKINKTILVGSAPNPHGIADIDELGIAQKYKRLPLVDSGLSFYSPMKAG 357

QY 331 YPLEHPDFRVKGVTSISADTHKKYGAAPKSSSLVLYSDKKYRNYQRFVDTMOGGIYAS 390

Db 358 YKMLPLDFRPGVTSISCTHKKYGFAPKSSVIMYRNSDRLMHQYVNPAMTGGTGLGSP 417

QY 391 TINGSPRGISACMAALMHGNGEYVETAKOIKTARFLKSELEKIRKIFVGNPOLS 449

Db 418 TLGSRGALVGCMAHVMNGENGYESQETVGAAMKFKKTYOENIPDLNMGNPRYS 477

QY 450 LIALGSRDPDIYRLSNLMTAKGWNLOLPPSIHFCITLLHARRVAIOFLDIRSVT 509

Db 478 VIFSSKTLNINHLEDRSLKSKGNHFNALOKPVALHMAFTRLSAH---VVDEICDILRTTV 534

QY 510 QIMK---NPKAKTTGMAIYMAQTVVDRNMVAELSLVFLDSLVS---STDYVTO 557

Db 535 QELKSSEKSPSPDGTSAIYGVSVTAGVADKLIVGFIDALYKLPGLPDTATK 589

RESULT 6

B69415

group II decarboxylase homolog - *Archaeoglobus fulgidus*C:Species: *Archaeoglobus fulgidus*

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999

C:Accession: B69415

R:Kien, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod

Glock, A.; Zhou, L.; Overbeek, R.; Goehay, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E

Nature 390, 364-370, 1997

A:Authors: Overbeek, T.; Cotton, M.D.; Spriggs, T.; Attiach, P.; Kaine, B.P.; Sykes,

Smith, H.O.; Moese, C.R.; Venter, J.C.

A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch

A:Reference number: A69250; WUID:98049343; PMID:9389475

A:Accession: B69415

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-488 <KLE>
A:Cross-references: GB:AE001012; GB:AE000782; NID:g2689335; PIDN:AA889922.1; PID:g264925
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 22.5%; Score 669; DB 2; Length 488;

Best Local Similarity 36.5%; Pred. No. 2.8e-44;
Matches 155; Conservative 83; Mismatches 171; Indels 16; Gaps 8;

```
OY 92 LNKTKDDISKNNMFLKVDKEYVKALPSQGLSSAVLEKREKSSMDAFQEGRASGV-Y 150
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 10 LNKGNHNSFEVKYIRITTKIMSPN-GSDAEGVLEKLEDAKADPEPHSRMMGHITY 68
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 151 SGEKLTLLVAYGDFAMSNPLHPDIPGLKIEAIVRIACSLFNGGPDSCCGTSGG 210
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 AGLKQVVELARAYLMYMDKTMLEDTCPSPILRMREVRMASSILNDEEVYGFYGG 128
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 211 TESTIMACKACRDIAFEK---GKTPETIVAPQSAANAANKASVYGMKIVVPLTKMMEV 267
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 129 TESTIMALKARE-KEREKGGNVVPELVLPATAPAWKSKSEYGMCLRAKLDDELRA 187
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 268 DVAMARRAISNTALVCTFPFPHGVIDPVPEVAKLAKYKIPHLVDACLGELIVEME 327
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 188 DVEYKELVGDKTAMIVASAPNPGVVDIKALSDIADVGLWHLVDACLGELIFPFR 247
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 328 KAGPFLHPDPRKGVTSISADTHKGYAPKSSLVLYSDKRYRNVFVDTDMQGIT 387
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 248 ELGEEKIP-DPFSVGVGHVSHISADFKYGLSPGASVILYRNAKIREGOIFVWASWPGYPL 306
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 368 ASPTAGSRPGISAAACAAALMHGENGVEATKQIITARLKSELEINIGIFVFGPQ 447
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 307 VNTAVLSTRAGSTLAAAVMSYLSGDTLAKTKLAKKRLDGLTEL-GLLELGSPE 365
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 448 LSLALGSRDPIYRLSNLMTAKGMNL-----NOLQPPSIHFCITLLHARKRAVLOFL 501
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 366 GAVLAFTSEBRNHLFVSTLMAEKGMVYQSPGSKTLGFPRLSHFVIRGHA--EYVDEFL 423
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 502 KDIRE 506
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 424 EDMRE 428
```

RESULT 7

659536
Group II decarboxylase homolog - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
C:Accession: G69536
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson, R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.; Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L. Nature 390, 364-370, 1997
A:Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artlisch, P.; Kane, B.P.; Sykes, S. Smith, H.O.; Moese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon, Pyrococcus furiosus.
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: G69536
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-414 <KLE>
A:Cross-references: GB:AE000946; GB:AE000782; NID:g2689269; PIDN:AA88962.1; PID:g264822
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 20.9%; Score 621.5; DB 2; Length 414;

Best Local Similarity 38.6%; Pred. No. 1.1e-40;
Matches 153; Conservative 68; Mismatches 152; Indels 23; Gaps 9;

```
OY 126 VLEKKEYSMDAFQEGRASGVY-SGEKLTLLVAYGDFAMSNPLHPDIPGLKRI 184
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 6 VLSLEKAESEDLNRTGRLEFAYVETGDENIRKAKALVFAEKNLIDFVFSAVFF 65
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 185 EAEIVRICSLFNGGPDSCGCVTSCTGESIIMACKACRDIAFEK--GKTPETIVAPQSAH 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

```
DB 66 EKEVGRARNIMHGA-AVSGFTGCTGSIMLAVAAADYRKKEGTAEVPEILLPISIH 124
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 243 AAFNKAASYFGMKIVRVPLTKMMEVDVAMRAISRNTAMLVCSPPPHGVIDPVEVA 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 125 PAFLLKAAVYLGKIVRLPV-KDAKGDVAPAEVAGKATALLASAPNMPFGTIDPEVEIA 183
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 303 KLAAYKIPHLVDACLGFLVEMKAGYPLEHPDFRVKGYTSISADTHKGYAPKSS 362
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 EIAERNVLLHVDACLGFLVPEFEMLEKIP-KEDFVEGVTSISLDAHKGYAPKAS 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 363 LVLYSDKKYRNQFVPDMDGCIYASPTLIGSRPGISACMAALMHGENGVEATKQ 422
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 VLFERDAELKCSMFVDVTSFGYFVNOAVLSSRPEGPLAAFAVITKLGVBGYELASK 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 423 IT---KTARFLKSELENIKGFVGNPOLSLIALGSRDPDIYRLSNLMTAKGMNL-- 475
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 ILSARDKLYRGLKS-----LGFESVGEVSSVLAMTNDVDLMGFVNMKKILGMQDLHOK 357
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 476 ---QLQPPSIHFCITLLHARKRAVLOFLKDIRESV 508
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 358 GLKEVDIPDNHILTLSPVH--DGAKEFEVDAKAL 391
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

RESULT 8

672452
Probable glutamate decarboxylase APE2267 - Aeropyrum pernix (strain K1)
C:Species: Aeropyrum pernix
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C:Accession: G72452

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Tanaka, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J. DNA Res. 6, 83-101, 1999
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339; PMID:10382966
A:Accession: G72452
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-454 <KAM>
A:Cross-references: DDBJ:AP000064; NID:g5105945; PIDN:BA81279.1; PID:g5105968
A:Experimental source: strain K1
C:Genetics:
A:Gene: APE2267
C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 19.1%; Score 567.5; DB 2; Length 454;
Best Local Similarity 35.2%; Pred. No. 2.1e-36;
Matches 139; Conservative 74; Mismatches 167; Indels 15; Gaps 9;

```
OY 126 VLEKKEYSMDAFQEGRASGVY-SGEKLTLLVAYGDFAMSNPLHPDIPGLKRI 184
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 4 VVKRLAETRAMDAREGGRLFTYLETGDPGVKEVSLRAFEKELDTNLDPTVRSALFF 63
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 185 EAEIVRICSLFNGGPDSCGCVTSCTGESIIMACKACRD-LAFKGIKTPETIVAPQSAH 243
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 64 EBEIVSFPASSLAGVGVGVYTTTGTESSILAAAMAHEWYKSLGSGSTRPGVAVQYVH 123
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 244 AFNKAASYFGMKIVRVPLTK-MMEVDVAMRAISRNTAMLVCSPPPHGVIDPVEVA 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 124 SVKKAARYLGMRLSTAPVDPGSKRYDIDSLVYDDRTAMVAVSAPNRYGVTDVRSVA 183
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 303 KLAAYKIPHLVDACLGFLVEMKAGYPLEHPDFRVKGYTSISADTHKGYAPKSS 362
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 184 EALSQORWLHVDACVGGFLLPEMRELGL-YSGAFVDEGVYSMDLHKTGSPKAS 242
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 363 LVLYSDKKYRNQFVPDMDGCIYASPTLIGSRPGISACMAALMHGENGVEATKQ 422
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 243 VLFERDGLKKSIFADLRMPGYPTINTVLSRSVAPLAAMAATVNLGRGVIELARK 302
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 423 IITARFLKSELENIKGFVGNPOLSLIALGSRD-PDIYRLSNLMTAKGMNLQ--- 478
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 303 AVEARDEIMRGLESI-GPRLAPIESTILSVLADDPADTLRPHANMSRGMWLG-LQPGV 360
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 479 ---PPPSIHFCITLLHARKRAVLOFLKDIRESVTO 510
||| : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
```

Db 361 EGIAPPNIHLTSPH--KLVSPOFLGDARASSSE 393

RESULT 9

hypothetical protein APE0020 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G72753

R:Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Hatake, Y.; Jin-no, K.; Takahawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: G72753

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-473 <KAW>

A:Cross-references: DDBJ:AP000058; NID:95103388; PIDN:BAA78929.1; PID:95103408

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0020

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 18.5%; Score 549.5; DB 2; Length 473;
Best Local Similarity 34.4%; Pred. No. 5, 8e-35;
Matches 135; Conservative 70; Mismatches 173; Indels 15; Gaps 8;

QY 126 VLEKLEKSSMDAFOGRASGTYS-GEKLTLLVKAAGDFAMSNPLHPIEPGLRK1 184
DB 13 VRELFLSSRDINPWTGRVTHVYDPCMDVKKASKALELYRDKTMLDFYVPSIIE1 72
QY 185 EAEIYRIACSLNNGSGDSCGVTSGTSESLMACACRDLAFKGIK-TPETIAPPSA243
DB 73 EKQLLGFAGHLTHAPBEGYGTFTYGTSESLIILAVLAARWRMRAGSGAKIMPTIAP132
QY 244 AENKASVYGMKIVRYPLTKM-MEVDVRRARRAISNTAMLCSTQPPHGVIDPPEVA302
DB 133 AFKAKAYLLGKVERPVSQVTLQADPAIEEKIDMDTYMTIASANDPYGSLDPVEDIG192
QY 303 KLAIVKIKPLHVDACIGFLIVFMKAGYPLEHPEDRVKAGVTSTADTKHKGYADKGS362
DB 193 DIAAARDVWLHVDACIGMVLAFASDAGEV-GKFDGVEGYVSFSVDMKKGYAPAKGS251
QY 363 ILVLSDKKRYNQFVDTMOGIVASPTIAGSRPGISAAACMAALMHGNGYVETATQ422
DB 252 ILFRARADKKPTIEVDSSMPGPIVYNQALISTRAGTLAAMAAVARTLGVEGYRELGM311
QY 423 IIKTARFLKSELENIGIFVGNPQSLIALSGRDFDIYRLSLMTAKGMNLNQD----478
DB 312 VLEARRRLOKGLSE-LGLEVLGRPKAGISLFTSDSDIDVVEVATRLGRAGW-VYQLOPKMK369
QY 479 ---PPPSIHFCITLLHARRVAIOFLKIDRESV 508
DB 370 HLGFTSIHLTSPPIHA--RVVDSFLAAVEESI 400

RESULT 10

D71084

hypothetical protein PH0937 - Pyrococcus horikoshii

C:Species: Pyrococcus horikoshii

C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000

C:Accession: D71084

R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Hatake, Y.; Hino, Y.; Yamamoto, S.; Sekita

M.; Ohikubo, Y.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; Oguchi

DNA Res. 5, 55-76, 1998

A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic

A:Reference number: A71000; MUID:98344137; PMID:9679194

A:Accession: D71084

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-383 <KAW>

A:Cross-references: GB:AP000004; NID:93236131; PIDN:BAA30034.1; PID:93257351

A:Experimental source: strain OT3

A:Note: this accession replaces an interim accession for a sequence replaced by GenBank

C:Genetics:

A:Gene: PH0937

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 17.4%; Score 518.5; DB 2; Length 383;
Best Local Similarity 31.1%; Pred. No. 1, 1e-32;
Matches 123; Conservative 83; Mismatches 165; Indels 25; Gaps 7;

QY 117 PSQGLSSSAVLEKLEKSSMDAFWQGRASGTYSGEKLTLLVKAAGDFAMSNPLHPI176
DB 4 PRIGLPEKVEVIELINEKTKKDLFFSSGKILGSMCTMPH--DLAIEVTRYKIDRNIGDPC60
QY 177 IEPGLKIEAEIYRIACSLFNGSPDSCGVTSGTSESLMACACRDLAFKGIKTPETIY236
DB 61 LHPGTREKEEVEIEMISDLH-LEKGHIVSGTEANILAVAFENLS--DVEKPELI116
QY 237 APOSAAAFNKAASYGMKIVRYPLTKMMEVDVRRARRAISRTALVCSSTPQPPHGVID296
DB 117 LPKSAHFSTIKAGEMGLVNAELNPDVTVDVRYDEAKISDNTIGIVGIAGTTGAGVD176
QY 297 PVPEVAKLAVKXKIPPLHVDACIGFLIVFMKAGYPLEHPEDRVKAGVTSTADTKHKG356
DB 177 DIPALSDLRADYGIPPLHVDAAFGFVIPPAGELGYELP-DFDEKLKGVSITIDPRKMGW235
QY 357 ARKSSLVLYSDKKRYNQFVDTMOGIVASPTIAGSRPGISAAACMAALMHGNGY416
DB 236 APYPAGIVFRRKKYKALSVLAPYLAGKQWQATITGRPGASVIAVWALLKHLGEEG295
QY 417 VEATKQIITARFLKSELENIGIFVGNPQSLIALSGRDFDIYRLSLMTAKGMNLN-475
DB 296 MRIVERAMLSRFAEIKKINNAWLVRPMLNIVFQIK--NLKVERELKSRGNGISA353
QY 476 ----QLOFPPIHFCITLLHARRVAIOFLADIRE 506
DB 354 HRCYIRIVFMP-----HVTREMIIEEFLDKLE 380

RESULT 11

G75102

group II decarboxylase PAB1578 - Pyrococcus abyssi (strain Orsay)

C:Species: Pyrococcus abyssi

C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000

C:Accession: G75102

R:anonymous, Genoscope

submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: Insights into archaeal chromosome s

A:Reference number: A75001

A:Accession: G75102

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-384 <KAW>

A:Cross-references: GB:AJ248286; GB:AL09836; NID:95458366; PIDN:CAB50124.1; PID:9545

A:Experimental source: strain Orsay

C:Genetics:

A:Gene: PAB1578

C:Superfamily: Escherichia coli glutamate decarboxylase

Query Match 17.3%; Score 514.5; DB 2; Length 384;
Best Local Similarity 30.6%; Pred. No. 2, 3e-32;
Matches 121; Conservative 86; Mismatches 164; Indels 25; Gaps 7;

QY 117 PSQGLSSSAVLEKLEKSSMDAFWQGRASGTYSGEKLTLLVKAAGDFAMSNPLHPI176
DB 5 PERGLPREVNLNLEDKTYVDLFFSSGKILGSMCTMPH--ELAIEVFARYIDRNIGDPC61
QY 177 IEPGLKIEAEIYRIACSLFNGSPDSCGVTSGTSESLMACACRDLAFKGIKTPETIY236
DB 62 LHPGTREKEEVEIEMISDLH-LEKGYHIVSGTEANILAVAFENIS--DAERPELI117
QY 237 APOSAAAFNKAASYGMKIVRYPLTKMMEVDVRRARRAISRTALVCSSTPQPPHGVID296

```

Db      118 LPKSAHSEFKIAGSMGLKVLMAELKODYADVADKVEAKISDNTIGIAGTGLGYVD 177
      297 PVPEVAKLAVKXKIPILHVDACTGFLTYFMEKAGYPLEHPDFRKGVTISADTHKXGY 356
      178 DIPALSDLARKYGIPLVHDAFGFVIFPAKSLGTDLP-DDDFKLGKVESTITIDPHKGM 236
      357 APKSSLVYSDKKYRNYQFVDTDWOGGIYASPTIAGSRPGGISACMAALMHFGNGY 416
      237 APIPAGGIIFRRKKYKLAISVLAFLYLAGKWMQATITGTIRPGASVLAVALIKHGFEGY 296
      417 VEATKOIITKARFLKSELENKGIFFVGNPQSLIALGSRPDIYRLSNLMTAGWNLN- 475
      297 REIVKKAWEISRMAEEIKKLNAMLVREPLNIVSFQTK--NLKVERELKRGWGISA 354
      476 -----OLQPPSIHFCITLLHARRVAIQFLKDIRE 506
      355 HRCYIRIVFMP-----HVTKEWVEFLRDIRE 381

```

RESULT 12

glutamate decarboxylase - Methanobacterium thermoautotrophicum (strain Delta H)

```

C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 03-Dec-1997 #text_change 22-Jun-1999
C:Accession: E69015
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
  Ki, S.; Church, G.M.; Daniels, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jivanli, N.
  J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-363 <MTH>
A:Cross-references: GB:AE000881; GB:AE000666; MUD:92622206; PIDN:AB85605.1; PID:9262221
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH116
C:Superfamily: Escherichia coli glutamate decarboxylase

```

```

Query Match      16.2%; Score 482; DB 2; Length 363;
Best Local Similarity 32.1%; Pred. No. 7.5e-30;
Matches 117; Conservative 77; Mismatches 159; Indels 12; Gaps 8;

      140 WQBSRAGTVYSGEKLTELIVKAYGDFAMSNPLHPDIFPGLRIEAIYIACSLFNGG 199
      3 YTSRIIGSMCTSSHPLAR---RYCCDFLESNLGDPGLFRGTRELESGVIGMLGELL-S-E 58
      200 PDSGCVTSGGTESILMACACRDLAIEKIGTPEIIVAPOSAHAFKASVFGMKIVRV 259
      59 PDAGHITITGTEANLAKMARARMA--GAKEPEIIVPKSAHSEFRKADILRLREA 115
      260 PLTKMMEVDVIRAMRATSRMTAMLCSTPQEPHGVIVPPEVAKLAKYKIPILHVDACTG 319
      116 ELDDIVADVDESARKLLISENTVAAGVAGTTELGRIIDPEELSEICDEDDHLHIDAFG 175
      320 GFLIVMEKAGYPLEHPDFRKGVTISADTHKXGYAPKSSVLVSDKKYRYQFVD 379
      176 GFILPFLRETAGALPE-FDKRLGCVSSITVDPHKMGIALIPSGCILFRDASYLD-ANSIE 233
      380 TDMOGGIYASPTIAGSRPGGISACMAALMHFGNGYVEATKOIITKARFLKSELENK 439
      234 TPYLETERQOS-TIVGTRTGASAAATWAIMKHMREGYRKALIRVAGVTRRLRDGLVELDY 292
      440 IFVGNPQSLIALGSRPDIYRLSNLMTAGWNLNOLQPPSIHFCITLLHARRVAIQ 499
      293 QLVV-EPGLINAVNHPAMGPHELARDLEELGMAVSVSCPPAIR-VLWPHIMEEHIEL 350
      500 FLKDI 504
      351 LIRDL 355

```

RESULT 13

group II decarboxylase homolog - Archaeoglobus fulgidus

```

C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Jun-1999
C:Accession: C69500
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dod
  R.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirsch, E
  Glodok, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
  Nature 390, 364-370, 1997
A:Authors: Overbeek, T.; Cotton, M.D.; Springs, T.; Artlich, P.; Kaine, B.P.; Sykes,
  Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing arch
A:Reference number: A69250; MUID:98049343; PMID:9389475
A:Accession: C69500
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-367 <KLE>
A:Cross-references: GB:AE000964; GB:AE000782; MUD:92689287; PIDN:AB89250.1; PID:9264
C:Superfamily: Escherichia coli glutamate decarboxylase

```

```

Query Match      12.8%; Score 380; DB 2; Length 367;
Best Local Similarity 27.7%; Pred. No. 7.1e-22;
Matches 108; Conservative 80; Mismatches 164; Indels 38; Gaps 11;

```

```

      126 VLEKIKREYSMDAFWQEGRAGTVYSGEKLTELIVKAYGDFAMSNPLHPDIFPGLRIE 185
      3 IIEELRAVRENDIYRSLVSSMCIVP-----HPVAVEAHNRHFIETNLGDPGIFRGYVE 57
      186 AEIVRIACSLFNGGPDSC---GCVTSGGTESILMACACRDLAIEKIGTPEIIVAPQSA 241
      58 AKIRLIGDILH-----CEPAGYICSGGTANIGIARARNVQK--ENPNIVIPKTA 109
      242 HAAKNKASVGMKIVRPLTKMMEVDVIRAMRATSRMTAMLCSTPQEPHGVIVPPEV 301
      110 HSESEKIGDILGVIKRAGVDEEYKVDGVEDLMDETVAIVIGAGTTELGQIDPIVEL 169
      302 AKLAVKXKIPILHVDACTGFLTYFMEKAGYPLEHPDFRKGVTISADTHKXGYA--PK 359
      170 SKLAEHREVELHVAAGGLVIFPMDN-----PYFPDQNGVSSITIDPHKMGATIPA 224
      360 GSSVLVYSDKKYRNYQFVDTDWOGGIYASPTIAGSRPGGISACMAALMHFGNGY 416
      225 GGII-----FRNESYLRALEVEPYLTSKTOFTLTGTIRPGASVLAVALIKSLGEGM 277
      417 VEATKOIITKARFLKSELENKGIFFVGNPQSLIALGSRPDIYRLSNLMTAGWNLN- 476
      278 REYVKNCKIKTRILVEEKRDL-GFEPVIEPVANVVSF--RTDEARIKEELYRMRWIST 334
      477 LQPPSIHFCITLLHARRVAIQFLKDIRE 506
      335 IREPKAIRF-VVMHVTVEEVIKNIISDFRK 363

```

RESULT 14

hypothetical protein M0050 - Methanococcus jannaschii

```

C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 22-Jun-1999
C:Accession: B64306
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blak
  rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
  Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese
  A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannasc
  A:Accession: B64306
A:Reference number: A64300; MUID:96337399; PMID:8688087
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-396 <BUL>

```

A:Cross-references: GB:U67463; GB:L77117; NID:g1590846; PIDN:AAB9031.1; PID:g1498811; C:Genetics;
A:Map position: REV52237-51047
C:superfamily: Escherichia coli glutamate decarboxylase

Query Match 12.4%; Score 369.5; DB 2; Length 396;
Best Local Similarity 27.9%; Pred. No. 5.3e-21;
Matches 103; Conservative 82; Mismatches 139; Indels 45; Gaps 13;

QY 113 VVALPQGLSSAVLEKLEKEYSSMDAFMQEGRASGVYSGEELTELKVAAYDFAMSNP 172
DB 1 MRNMQEGVSEKLEBELKRYSLDLKYEENIFGSMCSNVLPITRIYDI--FLETNL 57
QY 173 LHPDIFPGRLKRIAEIVRIACSLFNGGPDSCGCVTSGGTESILMACKACDLAEKGRK 231
DB 58 GDBGLKRGKRLLEKKAVALIGSLN-NKDAYGHIVSGGTANMALRCITNIREKRRKG 116
QY 232 ----TPEIVAPQSAHAFAFNKAASYFGMKIVRPVPLTKMMEVDVAMRAISR--NTAML 283
DB 117 LSKNEHPKTIIVPTAHFSFEKREMMDELYIVAPIKEDYTIDEKPVKDAVEDYDVGGIIG 176
QY 284 VCSTPQPPGVDPVPEVAKLAVKIKIPLHVDACLGGLIVEME---KAGYPLEHPDF 339
DB 177 IAGTTEL--GTIDNIELSKIAKENNIYIHVDAFGLVLPFLDDKYYKKKG--VNYKFD 232
QY 340 RVKGVTSISADTKHYGAPKSSLVLYSDKKYRNYOFVPTDMQGGIYASP-----T 391
DB 233 SL-GVDSITIDPHKMGHCPSPSGILFKDYGKRY--LDV-----APYLETRQAT 281
QY 392 IAGSRPGISACMAALMHFENGVEATKOIITARFLKSELE--NKGIFVFGNPOLS 449
DB 282 ILGTRVQFGACGYAVLRVYLRGQGRIVNECMENLYLYKKLKENNFKPVI--EPILN 338
QY 450 LIALGSRDF 458
DB 339 IVAIEDEY 347

RESULT 15

D84192
glutamate decarboxylase [Imported] - Halobacterium sp. NRC-1
C:Species: Halobacterium sp. NRC-1
C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C:Accession: D84192
R:Ng, W.V.; Kennedy, S.P.; Mahairs, G.G.; Bergquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.;
Leitauer, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jabc
Jung, K.H.; Alam, M.; Freltas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A:Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ehardt, H.; Lowe, T.M.; Li
A:Title: Genome sequence of Halobacterium species NRC-1.
A:Reference number: AB4160; MUID:20504483; PMID:11016950
A:Accession: D84192
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-355 <STO>
A:Cross-references: GB:AE004437; NID:g10579954; PIDN:AA618904.1; GSPDB:GN00138
C:Genetics:
A:Gene: gad

Query Match 10.4%; Score 308.5; DB 2; Length 355;
Best Local Similarity 27.5%; Pred. No. 2.6e-16;
Matches 94; Conservative 64; Mismatches 155; Indels 29; Gaps 9;

QY 167 FANSNPLHPDIFGLKRIEAEIVRIACSLFNGGPDSCGCVTSGGTESILMACKACRDLAF 226
DB 35 FLATNPDDPTPYPAVARERDAVALIGEIV-GLSSPHGYIAGGTETANLQAVRAARNRAD 93
QY 227 EKGITPEIYAPQSAHAFAFNKAASYFGMKIVRPVPLTKMMEVDVAMRAISRNTAMLCVS 286
DB 94 ADAV---NVYAPASAHSEFQKADVLGVELRLAPTDGDHRADVAADVADYDGDYAVYGV 150
QY 287 TQGFPHGVDPVPEVAKLAVKIKIPLHVDACLGGLIVFMEKAGYPLEHPDFPRKGVTS 346

DB 151 AGTTEYGRVDPPIPALADIAGVDANLHVDAAMGCVLPF-----TDHDMSEFADAPVNT 203
QY 347 ISADTKHYGAPKSSLVLYSDKKYRNYOF---FVDTDMQGGIYASPTIAGSRPGISA 402
DB 204 MALDPHMGAPVPAGGFLARDEPITDALAIETPILESIDT-----PTIGTRSGAGVA 257
QY 403 ACMAALMHFENGVEATKOIITARFLKSELENIGIFVFGNPOLSLIAGSRDPDIYR 462
DB 258 GALASIRALMPDGYREYERTQGAETLAELA-ARGYDVV-DPELPVLAADPDADAEQA 315
QY 463 LSNLMTAKGWNLODPSPSIHFCITLLHARKKVAIOFLKDI 504
DB 316 LRE-----EGWRISRTASDALRVVCMF--HYTREMLAFLDDV 351

Search completed: October 6, 2003, 13:56:25
Job time : 31 secs

